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- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

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1, Appli 1, Appli 18, Appl

Sequence 136, Magagemence 57, Al Sequence 17, App Sequence 7, App Sequence 7, App Sequence 123, Magagemence 11, App Sequence 12, App Sequence 12, App Sequence 12, App Sequence 12, App Sequence 13, App Sequence 31, App Sequence

US-07-945-283-1 US-09-732-025-3 US-08-804-255-3 US-08-804-198-1 US-08-439-725A-1 US-08-867-471-1

3, Appli 3, Appli Appl i

318,

Sequence

US-09-920-048-3 US-09-149-476-318 US-09-050-159-129 US-08-705-245-18 PCT-US96-06664-1 US-09-813-819-3

ALIGNMENTS

1, Appli 3, Appli Appli Appli Appli

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STATE: VA
COUNTRY: USA
Z119: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIble
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELease #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                  APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
AURESPONDENCE ADDRESS:
ADDRESSE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECHONICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEPHONE: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                              Sequence 14, Application US/08232463; Patent No. 5670367; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 899149'
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.2%;
 TYPE: nucleic acid
STRANDEDNESS: single
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US-08-232-463-14
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                                                                                March 30, 2003, 09:12:13; Search time 33.7584 Seconds (without alignments) 9093:534 Million cell updates/sec
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Sequence 13, Sequence 1, Al
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Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-232-463-114
US-09-441-340-27
US-09-668-101-5
US-08-658-136-2
US-08-658-136-2
US-08-58-136-1
US-08-234-638-3
US-08-4280-3
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-09-461-697-151
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JS-09-165-264-13
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-08-751-344B-1
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                                                                                                                                                                                                                         441362 seqs, 153338381 residues
                                                                                                                                  US-09-691-220-3_COPY_5000_6000
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                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                             - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length DB
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7218
2378
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1403
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Perfect score:
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                                                             OM nucleic
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Length 7218;

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DB

52;

Score

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US-07-728-220C-2
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                                                                                                                                                                                                                                                         373 TCAGCCAGGCTGGCCTGGGAAGTGGTGCCCAGGCACTACTAAGAGCCCAGGAAAGCCCTGC 432
                                                                                                                                                                                                                                                                                                                             433 CAAGGTTGTTGGCCTAGTTCCCTGTCATCAGCCCCCTAGCAGCCCCCACTGTGTTGTGCAG 492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Matsuo, Hisayuki
APPLICANT: Matsuo, Hisayuki
APPLICANT: Manamino, Naoto
TITLE OF INVENTION: NOVEL HYSIOLOGICALLY ACTIVE PORCINE
TITLE OF INVENTION: PEPTIDE (CNP-53)
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHAMAN DARBY & CUSHAMAN
STREET: ELEVENTH FLOOR, 1615 1 STREET. N.W
                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/728,221B
FILING DATE: 19910712
CLASSIFICATION: 530
 Pred. No. 2.7e-05;
06; Mismatches 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WTS/9437/91817/KIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 12, Application US/07728221B Patent No. 5340920 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORREY/AGENT INFORMATION:
NAME: SCOTT, WATSON T.
REGISTRATION NUMBER: 26,581
REPERENCE/DOCKET NUMBER: WTS/:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELESA: (202) 822-0944
TELEX: (201) 822-0944
ILENEX: (201) 822-0944
SEQUENCE CHARACTERISTICS:
 l Similarity 4.3%; Pred
16; Conservative 206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 549 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WASHINGTON
Best Local Similarity
Matches 16; Conserv
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ZIP: 20036-5601
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149 CTGTTCTCAGGCCTCTCAGC----CTGTCTGATTTGCTTGTCTGGCCTGGGGAGAATGAG 204
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                                                                                                                                                                                                                                                                                                                                      265 GGTCAGGAGAATCTGCTGGGCTGGGGATGGTGGGGCATCAACTGTCCCATTGCTGCA 324
                                                                                                                                                                                                                                                                                                                                                                                                        325 GGCTGGTCTTGGGGCAGGGAAGGGGATGGGGGGCCATAGCAGTGCTGGTCAGC 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66 CGGAGCAGACTGGCCGGGTGCGGGCGCGAGTGCTGCTGCGGCG 14
                                                            Length 549;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: FUCHIMURA, KAYOKO
APPLICANT: TANARAGI, YASUNORI
TITLE OF INVENTION: PORCINE CNP GENE AND PRECURSOR PROTEIN
NUMBER OF SEQUENCES: 22
                                                                                               0; Mismatches 144; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                          Score 44.6; DB 1;
Pred. No. 0.0013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S: CUSHMAN, DARBY & CUSHMAN ELEVENTH FLOOR, 1615 L STREET, N.W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: WTS/9437/91816
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)861-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19910712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/07728220C Patent No. 6020168
    DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: MATSOO, HISAVUKI
APPLICANT: KANGAWA, KENJI
APPLICANT: TANAKA, SHOJI
                                                        4.5%;
Best Local Similarity 49.5%;
Matches 145; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, WATSON T.
REGISTRATION NUMBER: 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (202)822-0944
TELEX: 671 4627 CUSH
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  549 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEIC ACID
EDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: CUSHMA
STREET: ELEVENTH
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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; MOLECULE TYPE:
US-07-728-221B-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 3
US-07-728-220C-2/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
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175 GATTTGCTTGTCTGGCCTGGGGAGAATGAGGTGGGAGAAAACCAGGCCAGGGCAGTTGGT 234
                                            295 GGTGTGGGCATCAACTGTCCCATTGCTGCAGGCTGGTCTTGGGGGCAGGGAAGGGGATGGG 354
                                                                                                                                                                                                                                               355 GGGCCATAGCAGTGCTGGTCAGCCAGGCTGGCCTGGGAAGTGGTGCCCCAGGCACTACTAA 414
                                                                                                                                                                                                 262 GGGCCGGCGGGCAGACTGGCAAACCGAGCAGAGCAGACTGGCCGGGCTGCGGTGCGGG
                                                                                              GTTGGAGTGAAGAGCAGACGGCGGTGGGGAGGTCAGGAGAGAATCTGCTGGGCTGGGGAT
                                                                                                                                                                                                                                                                                                                        415 GAGCCAGGAAAGCCCTGCCAAGGTTGTTGGCCTAGTTCCCTGTCATCAGCCGCC 468
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Pred. No. 0.16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Satent No. 50,000.
GENERAL INFORMATION:
APPLICANT: DCRIFFLINGER, F.
APPLICANT: SCHEFLINGER, F.
APPLICANT: FALKNER, F. G.
APPLICANT: FALKNER, F. G.
APPLICANT: FALKNER, F. G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSEE: Foley & Lardner
F: 1800 Diagonal Road, Suite 500
Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EP 91 114 300.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 14, Application US/08232463 Patent No. 5670367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29,768
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.9%;
1.6%; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: EP 91
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: REG
NUMBER OF SEQUENCES: 5:
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-232-463-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-232-463-14
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                                                                         89 TGGCTCACCCCTCTGCCTCTGGCCTCACCCAGGCCCCCCAACCCCGCCCCCCCAGCAG 148
                                                                                                149 CTGTTCTCAGGCCTCTCAGC----CTGTCTGATTTGCTTGTCTGGCCTGGGGAATGAG 204
                                                                                                                                                                      GTGGGAGAAAACCAGGCCAGGGCAGTTGGTGTTGGAGTGAAGAGCAGACGCGGTGGGGA 264
                                                                                                                                                                                                                                                                                                   265 GGTCAGGAGAATCTGCTGGGCTGGGGATGGTGTGGGCATCAACTGTCCCATTGCTGCA 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                             325 GCCTGGTCTTGGGGCAGGGAAGGGGATGGGGGGCCATAGCAGTGCTGGTCAGC 377
                                                                                                                                                                                                                                                                                                                                                                                                    Length 1894;
   DB 3; Length 549;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: TANAKA, SHOJI
APPLICANT: FUCHIMURA, KAYOKO
APPLICANT: TAWARAGI, YASUNORI
TITLE OF INVENTION: PORCINE CNP GENE AND PRECURSOR PROTEIN
NUMBER OF SEQUENCES: 22
 Score 44.6; DB 3; Length 5
Pred. No. 0.0013;
0; Mismatches 144; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/728,220C
FILING DATE: 19910712
FILING DATE: 19910712
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, WATSON T.
REGISTRATION NUMBER: 26,581
REFERENCE/POCKET NUMBER: 26,581
REFERENCE/POCKET NUMBER: WTS/9437/91816
TELEPHONE: (202)861-3000
TELEFA: (202)862-0944
TELEFA: 671 4627 CUSH
INFORMATION FOR SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
STREET: ELEVENTH FLOOR, 1615 L STREET, N.W.
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 39.6; DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 0.06
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/07728220C
Patent No. 6020168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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4.5%;
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TYPE: NUCLEIC ACID
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KANGAWA, KENJI
                                    Matches 145; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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'RY: USA
20036-5601
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Matches 135; Conserv
                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-07-728-220C-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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 Ouery Match
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2664 TTTTTTTTTGCTGCGAGACGTGCGGTGCGGACAACTCACGGTGATAGTGGGGGGG 2605
  634 GACTATTGTCCAGTTGGCTGGACTGGGGTGGGCTGGGTTGGGTTGGGTTGGGCTTGGGCTT 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 CAGGCCCCCCCAACCCCGCCCCCCCAGCAGCTGTTCTCAGGCCTCTCAGCCTGTCTGATTT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: (1999)..(3400)
OTHER INFORMATION: label - PRAC1, "promoter region of rice actin gene
OTHER INFORMATION: - contains an intron in the leader"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Artificial Sequence: other nucleic pMV71"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3' untranslated
Agrobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240 AGTGAAGAGCAGACGGCGGTGGGGAGGTCAGGAGAAATCTGCTGGGCTGGGGATGGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2544 GGGCTTGCTATGGATCGTGGATAGCACTTTGGGCTTTAGGAACTTTAGGGGTTG 2491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGCATCAACTGTCCCATTGCT-GCAGGCTGGTCTTGGGGCAGGGAAGGGGATG 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 38; DB 4; Length 4032;
Pred. No. 0.24;
0; Mismatches 115; Indels
                                                               Ncol, "Ncol recognition site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY: misc_feature
; LCCATION: (4016)..(4021)
; CTHER INFORMATION: label = KpnI, "KpnI recognition site"
0S-09-068-101-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3'nos, "region containing
nopaline synthase gene of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       barstar, "barstar
                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: PLANT GENETIC SYSTEMS N.V.
TITLE OF INVENTION: Improved Barstar Gene
FILE REFERENCE: 2121-139P;
CURRENT APPLICATION NUMBER: US/09/068,101
CURRENT FILING DATE: 1998-08-26
EARLIER APPLICATION NUMBER: EP 96202446.9
EBARLIER FILING DATE: 1996-09-03
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTI VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   = 3'nos, "region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of
OTHER INFORMATION: acid, "plasmid
                                                                                                                                                             US-09-068-101-5/c
; Sequence 5, Application US/09068101
; Patent No. 6372960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 3.8%;
Best Local Similarity 50.4%;
Matches 118; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: (3677)..(4003)
OTHER INFORMATION: label = 3
OTHER INFORMATION: end of
OTHER INFORMATION: T-DNA"
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LOCATION: (3401)..(3676)
OTHER INFORMATION: label
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: (3399)...(3404)
OTHER INFORMATION: label
FEATURE:
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                                                                        62 AAGTTAGCACAACAAAGGGCTGCTTTGTGGCTCACCCCCTCTGCCTCCTGGCCTCACCCA 121
                                                                                                                                                                                                 GGCCCCCCAACCCCCCCCCCCCAGCAGCTGTTCTCAGGCCTCTCAGGCCTGTCTGATTTGC 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126 CCCCAACCCCGCCCCCCAGCAGCTGTTCTCAGGCCTCTCAGGCTGTCTGATTTGCTTGT 185
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                                    2 GATCTCCCCCCCCCCCACCAGTCTGGATTGTCTATTGTTACTGCTTTTACGTCTTGGAAA 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence:expression OTHER INFORMATION: cassette comprising a plant promoter linked to OTHER INFORMATION: intron, a sequence encoding an AMPA acetyl OTHER INFORMATION: transfer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4; Length 2378;
  64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Phosphonate Metabolizing Plants
FILE REPERENCE: 38-21(15303)
CURRENT APPLICATION NUMBER: US/09/441,340
CURRENT FILING DATE: 1999-11-16
BARLIER APPLICATION NUMBER: 60/108,763
BARLIER FILING DATE: 1998-11-17
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 38.4; DB 4;
Pred. No. 0.15;
0; Mismatches 111;
Conservative 124; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 27, Application US/09441340
Patent No. 6448476
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.8%;
ilarity 50.9%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; NAME/KEY: terminator
; LOCATION: (2114)..(2369)
US-09-441-340-27
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                                                                                                                                                                                                                                                                                 TTGTCTGGCCT 192
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Best Local Similarity
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'n
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COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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Best Local Similarity 52.2%;
Matches 83; Conservative
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                                                                                                                                       STATE: MASSACHUSETTS
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MOLECULE TYPE:
                                                                                                                                                                            01701
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                                                                                                                                                        COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     259 IGGGGAGGTCAGGAGAATCTGCTGGGCTGGGGATGGTGGGGCATCAACTGTCCCATT 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 53526;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76; Indels
                                                                                                                         APPLICANT: CONNORS, TIMOTHY D
APPLICANT: DACKOWSKI, WILLIAM
APPLICANT: GERMINO, GREGORY
APPLICANT: OIAN, FENG
TITLE OF INVERTION: POLYCYSTIC KIDNEY DISEASE GENE
NUMBER OF SEQUENCES: 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35540 GGGGGAGGGAAAGGAGGAGGAAGGAGGAGGAGGGG 35502
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               319 GCTGCAGGCTGGTCTTGGGGCAGGGGAAGGGGGATGGGGGGG 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 37.4; Di
Pred. No. 1.1;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GEN4-17.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/658,136
                                                                                                                                                                                                                                                           SEE: GENZYME CORPORATION
: ONE MOUNTAIN ROAD
FRAMINGHAM
                                                             KLINGER, KATHERINE W
LANDES, GREGORY M
BURN, TIMOTHY C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: LASSEN, ELIZABETH
REGIESTRATION NUMBER: 31,845
REFERENCE/DOCKET NUMBER: GEN4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 508-872-8400
                   Sequence 2, Application US/08658136
Patent No. 6071717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08658136
Patent No. 6071717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KLINGER, KATHERINE W
LANDES, GREGORY M
BURN, TIMOTHY C
CONNORS, TIMOTHY D
                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 508-8/2-5412
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 53526 base pairs
TYPE: nucleic acid
cTRENDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: DNA (genomic) US-08-658-136-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 52.23
Matches 83; Conservative
                                                                                                                                                                                                                                                                                                                       STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 01701
                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: GENZYME CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: KLINGEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE
US-08-658-136-2/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-658-136-1/c
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APPLICANT:
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Sequence 3, Application US/09534638

Patent No. 6520038

GENERAL INFORMATION

GENERAL INFORMATION

APPLICANT: Panula, Pertti A.J.

APPLICANT: Panula, Pertti A.J.

APPLICANT: Panula, Pertti A.J.

APPLICANT: Panula, Johanna

TITLE OF INVENTION: From therapy and diagnosis

FILE REFERENCE: 2530-104

CURRENT APPLICATION NUMBER: US/09/534,638

CURRENT FILING DATE: 1900-03-27

EARLIER REPLICATION NUMBER: 09/365755

EARLIER FILING DATE: 1999-08-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           259 TGGGGAGGTCAGGAGAAATCTGCTGGGCTGGGGATGGTGTGGGCATCAACTGTCCCATT 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OFTWATING SITEM:
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/658,136
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LASSEN, ELIZABETH
REGISTRATION NUMBER: 31,845
REFERENCE/DOCKET UNBER: 31,845
RECISTRATION NUMBER: 31,845
RECISTRATION NUMBE
APPLICANT: GERMINO, GREGORY
APPLICANT: GIAN, FENG
TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
WUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSE: GENZYME CORPORATION
STREET: ONE MOUNTAIN ROAD
CITY: FRAMINGHAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          319 GCTGCAGGCTGGTCTTGGGGCAGGGAAGGGGATGGGGGG 357
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us-09-691-220-3_copy_5000_6000.rni

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1060 AGAAAGGGCAAGGGCCCCTGTGAGATCAGAGAGTGGGGGTGCAGGGCAGGAGGAACTGA 1119
                                   373 TCAGCCAGGCTGGCCTGGGAAGTGGTGCCCAGGC 406
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                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Human
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                                                                                                               RESULT 12
US-09-754-250-3/c
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                                                                                                                                                                                        152 TICTCAGGCCICTCAGCCTGTCTGATTTGCTTGTCTGGCCTGGGGAGAATGAGGTGGGAG 211
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                                                                                                 Gaps
                                                                                                                          92 CTCACCCCTCTGCCTCTGGCCTCACCCAGGCCCCCCAACCCGGCCCCCCAGCAGCTG 151
                                                                                                                                                                                                                     316 GGATTACAGGCACACACCACTATGCCCGGCTAATTTTTGTAGGGGGAGTAGAGATGGGGT 257
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                                                                  Length 2480;
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                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Boone, Thomas C.
APPLICANT: Miller, Allan L.
TITLE OF INVENTION: DNA Encoding Canine Granulocyte Colony
TITLE OF INVENTION: Stimulating Factor (G-CSF)
CORRESPONDENCE: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
                                                                                             79; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches 111; Indels
                                                                                                                                                                                                                                                    212 AAAACCAGGCCAGGCAGTTGGTGGAGTGAAGAGCAGACG 254
                                                                                                                                                                                                                                                                                  256 TTCACCATGTTGGCCAGGCTGGTCTTGAACTCCTGACCTCAAG 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 36.4; DB 1;
Pred. No. 0.63;
                                                                  DB 4;
                                                               Score 36.6; D
Pred. No. 0.5;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Amgen Inc.
1840 Dehavilland Drive
                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/08428732 Patent No. 5606024 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Crandall, Craig A.
REFERENCE/DOCKET NUMBER: A
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.68;
                                                              3.7%;
ilarity 51.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 3070 base pairs
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COMPUTER READABLE FORM:
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                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid
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                                                            Query Match
Best Local Similarity
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                                                                                             84;
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                               US-09-534-638-3
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                 ORGANISM:
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TYPE: DNA
                                                                                             Matches
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39374 TCGCAGGGCCGCTCTCAGAGCCTCCACCTGTCTGATCGCACCCTGTTTCCCCGCCACC 39315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80 GCTGCTTTGTGGCTCACCCCCTCTGCCTCCTGGCCTCACCCAGGCCCCCCAACCCCGGCC 139
                                                                                                                                                                                                           GENERAL INFORMATION:

APPLICANT: WEL, MING-Hui et al

APPLICANT: WEL, MING-Hui et al

TITLE OF INVENTION: ISOLATED HUMAN PHOSPHODIESTERASE

TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN

TITLE OF INVENTION: PHOSPHODIESTERASE PROTEINS, AND USES THEREOF

FILE REFERENCE: CL001063

CURRENT APPLICATION NUMBER: US/09/754,250

CURRENT APPLICATION NOMBER: 2001-01-05

NUMBER OF SEQ ID NOS: 5

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              260 GGGGAGGICAGGAGAAICTGCTGGGCTGGGGATGGTGGGGCATCAACTGTCCCATTG
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APPLICANT: ABRAHAM, J.D.
APPLICANT: ABRAHAM, J.C.
ANDRES OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39134 GGACAGGCCTGGAGCAGTCGCCCATCTGCGAGGGAGA 39097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches 181;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   379 AGGCTGGCCTGGGAAGTGGTGCCCAGGCACTACTAAGA 416
1120 ACAGCCTGGCAGGACATGGAGGGAGGGGAAAGAC 1153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 36.4; D
Pred. No. 2.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (1)...(111282)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                  Sequence 3, Application US/09754250 Patent No. 6376225
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Search completed: March 30, 2003, 13:56:22 Job time: 174.758 secs
                                                   Query Match 3.5%;
Best Local Similarity 46.3%;
Matches 114; Conservative
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     154 CICAGGCCTCTCAGCCTGTCTGATITGCTTGTCTGGGGGGGGAGAATGAGGTGGGAGAA 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            436 GGCCGGCTCCCCCCCGGACTGATGTCGCGCGTTGCGTGTTGTGGCCGAAGCCGCCGAA 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence:Primer sequence US-09-165-264-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.5%; Score 35.4; DB 4; Length 1969; ilarity 50.3%; Pred. No. 1; Conservative 0; Mismatches 86; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Unity of the property of the proper
                                                                                                                                                                                                                          COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FSSESSO for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/098,628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 21900-20089.10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7, Application US/09165264
Patent No. 6197510
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K
REGISTRATION NUMBER: 33,943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Coding Sequence LOCATION: 970...1434
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1969 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 706141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                              Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                               COMPUTER READABLE FORM:
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Palo Alto
                                                                                                       94304-1018
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ses 87; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                           USA
                                                                                                                                                                                      MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-098-628-1
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                                                                                                                             248 GCAGACGGCGGTGGGGAGGTCAGGAGAATCTGCTGGGCTGGGGATGGTGGGGATCA 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      188 GGCCTGGGGAGAATGAGGTGGGAGAAAACCAGGCCAGGGCAGTTGGTGTTGGAGTGAAGA 247
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                                                                                                                                                                                                                                                               308 ACTGTCCCATTGCTGCAGGCTGGTCTTGGGGCAGGGAAGGGGATGGGGGGCCATAGCAGT
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      Length 320;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 3.4%; Score 34; DB 4; Length 320; Best Local Similarity 47.6%; Pred. No. 1.2; Matches 100; Conservative 0; Mismatches 110; Indels
Score 34.8; DB 4; Length 3
Pred. No. 0.7;
0; Mismatches 132; Indels
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Sequence 13, Application US/09165264

Fatent No. 6197310

GENERAL INFORMATION:

APPLICANT: Vinayagamoorthy, Thuralayah

TITLE OF INVENTION:

HILE REFERENCE: 44747

CURRENT PAPLICATION NUMBER: US/09/165,264

CURRENT FILING DATE: 1998-10-01

NUMBER OF SEQ ID NOS: 14

SEQ ID NO 193

LENGTH: 320
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2000US-0226681
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                                                                14-AUG-2000;
18-AUG-2000;
22-AUG-2000;
22-AUG-2000;
23-AUG-2000;
30-AUG-2000;
30-AUG-2000;
30-AUG-2000;
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01-SEP-2000;
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02-0CT-2000; 20
02-0CT-2000; 20
13-0CT-2000; 20
13-0CT-2000; 20
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08-NOV-2000;
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Db 104439 CCGGCCGSNNNDNNCCGCBGGCCBGGCGCCGCCGGCCSNNNDNNCCGCBGGCCBGGG 104498
                                    Db 104559 GGGCGCCCGCCGCCSNNNDNNCCGCBGGCCBGGCCGCCCCSNNNDNNCCGCBGGCCBG 104618
                                                                                                                       Db 104679 GCCSNNNDNNCCGCBGGCCBGGCCGCSNNNDNNCCGCBGGCCBGGCGGGSNNNDNNC 104738
                                                                                                                                                                                                                                                                                                                                                       Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidabetic; antinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein; ds.
                                                                                                                                                                                                                                                                                                                                  Human ovarian and breast cancer associated polynucleotide SEQ ID NO 1003.
                       671 GGCCCGGCCTGGGTGGGGTGTGTTAAGGGGAGGACACCGGGACCACCCCCCCTCTTCC 730
                                                                731 CCGCCCCACCACCTCCACCACGGCTTCGCTCGGCCAGGGACTGACCAAACCTTGGGG 790
                                                                                                                                                   851 CCTCGCAGCCCCCTCTCTCCTGTACTCGGCGTCCCTCTGTACTCTGTGTACTCCTCAT 910
                                                                                                         Db 104739 CGCBGGCCBGGCGCSNNNDNNCCGCBGGCCBGGCCBGGCGGGG 104788
                                                                                                                                                                                            911 CIGGAGCCITICCCCCTTCCTGCTTCTCTCTCCTCCCCCTTCCCAGG 960
                                                                                                                                                                                                                                                                    ABA08208 standard; DNA; 13862 BP
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20000S-0205515
2000US-0209467
2000US-0214886
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2000US-0218290.
2000US-0220963.
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2000US-0216647
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07-JUL-2000;
07-JUL-2000;
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ABA08208
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08-NOV-2000; 08-NOV-2000; ñ

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The invention relates to novel genes (ABA07454-ABA08224) and proteins (ABB10743-ABB10980) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (C) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated ovarian and/or breast cancer related nucleic acids and polypeptides, useful for diagnosing, treating and/or preventing human diseases and disorders, particularly ovarian and/or breast cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 1003; 577pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 13862 BP; 3188 A; 3560 C; 4465 G; 2649 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         epilepsy; and (f) infection and parasitic infections.
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                                                                                                                                   -NOV-2000;
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Human; reproductive system related antigen; reproductive system disorder;
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                     640
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                                                                                                                                                                                               GGGAGGACAC - CGGGACCACCCCCTCTTCCCCGCCCCACCACCTCCTCCACCACGGCTT 759
                                                                5904 CCATGGGGCGGACGGGGGGGCTCTATGGGGTGGGAGGGGCTTGGTCGGGAGGGGCGGGA
                                                                                                                                                                                                                                           760 GGCTCGGCCAGGGACTGACCAAACCTTGGGGGAGCCTGGGAGCCGGAACTGGTACAAGGG
                                                                                                                                                                                                                                                                                      820 GAGGACGCCCCCCCTCTTCCGTCCTTGTCCCTCGCAGCCCCCTCTCCTCTTGTACTC
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                                                                                                                                                     GGCGTCCCTCTGTACTCTGTACTCCTCATCTGGAGCCTTTCCCCCCTTCCTGCTTCTCT
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260;
 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                 7263 CITCCCAGICICIT 7276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancer; gene therapy; ds
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18-APR-2000;
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232;
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                    461
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Matches
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2000US-0216880

07-JUL-2000;

Length 13862;

Score 54; DB 22; Pred. No. 0.013;

5.4%;

Query Match Best Local Similarity

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2000US-0239935
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The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 5477; 1297pp + Sequence Listing; English.
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47.0%; Pred. No. 0.013;
Live 0; Mismatches 260; Indels
                          2000US-0244617.
2000US-0246474.
2000US-0246475.
2000US-0246476.
2000US-0246477.
2000US-0246477.
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Best Local Similarity 47.0
Matches 232; Conservative
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20-0CT-2000; 20-0C
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17 - NOV - 2000;
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Gaps

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2000US-0224518.
2000US-0224519.
2000US-0225213.
2000US-0225214.
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2000US-0229345.
2000US-0229509.
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2000US-0230437.
2000US-0230438.
2000US-0218290.
2000US-0220963.
2000US-0220964.
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000US-0232081
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                                                                                                                            641 GAGTTCAGCCGCATTGCATTAGGCAAATGAGGCCCGGCCTGGGGTGGGGGGTGTGTTAAG 700
            6904 CCATGGGGGGGGGGGGGGGTCTATGGGGTGGGGCTTGGTCGGGAGGGCCGGA 6963
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Human reproductive system related antigen DNA SEQ ID NO: 10204
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for use in mammalian vaccine against Aujeszky's disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition
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                                                                                                                                                                useful
of
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                                                                                                                                                                                                                                                                                                                                                                                            Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.
                                                                                                                          Gaps
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                                                                                                 Length 4897;
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                                                                           Sequence 4897 BP; 594 A; 2052 C; 1495 G; 756 T; 0 other;
                                may be used as a vaccine to provide 19s, with resistance against Aujeszky's
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Pred. No. 0.036;
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                                                                                                 5.2%; Score 51.6; 55.6%; Pred. No. 0.
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            Disclosure; Fig 1; 21pp; English.
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05-SEP-2000; 2000DE-1044543.
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                                             e.g. pigs,
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                                The polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 12;
                                                                                                                                                                                                                                                                                                                                ABQ52496;
                                                        disease.
                                                                                                 Query Match
                                                                                                                                                                                                                                                                                       RESULT 14
ABQ52496/c
                                                                                                                       Matches
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classes of oligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously. ABO13410-ABO54121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in the disclosure of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            708 CACCGGGACCACCCCCCTCTTCCCCGCCCCACCACCTCCTCCACCACGGCTTCGCTCGGC 767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oligonucleotide for detecting cytosine methylation SEQ ID NO 39088.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            768.CAGGGACTGACCAAACCTTGGGGGAGCCTGGGAGCCGGAACTGGTACAAGGGGAGGGGACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCCCCTTCCCAGGCTGCCCCACTTGCCTGTCCACATGCCGCCTCTCCCTCTC 1000
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                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 600 BP; 26 A; 51 C; 478 G; 44 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  á
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABQ52497 standard; DNA; 600
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05-SEP-2000; 2000DE-1044543.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 48.5
Matches 142; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (EPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-371829/40.
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methylation of a particular cytosine in a motif 5'-cp6'3', present in a genomic sample of DNA. The sample is treated chemically to convert of genomic sample of DNA. The sample is treated chemically to convert or cytosine (C) but not methylated C, to unacil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used (i) for diagnosis and/or prognosis of side effects of the rapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation of call or tissue cypes and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously.

ABO13410-ABO54121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in
                                                                                                                         invention describes a novel method for determining the degree
                                                                Claim 12; 56pp + Sequence Listing; 56pp; German.
amplicons from chemically treated DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the disclosure of the invention
                                                                                                                             This
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Sequence 600 BP; 44 A; 478 C; 51 G; 26 T; 1 other;

ö 708 CACCGGGACCACCCCCTCTTCCCCGCCCCACCACCTCCACCACGGCTTCGCTCGGC 767 768 CAGGGACTGACCAAACCTTGGGGGAGCCTGGGAGCCGGAACTGGTACAAGGGGAGGACGC 827 828 CCGCCCTCTTCCGTCGTTGTCCCTCGCAGCCCCTCTCTCCTGTACTCGGCGTCCC 887 441 Gaps ó 948 CCCCCTTCCCAGGCTGCCCCACTTGCCTGTCCACATGCCGCCTCTCCCTCTC 1000 Query Match 5.1%; Score 51.4; DB 24; Length 600; Best Local Similarity 48.5%; Pred. No. 0.028; Matches 142; Conservative 0; Mismatches 151; Indels 0 ŏ g ò g õ ద ద δ ò

Search completed: March 30, 2003, 10:05:51 Job time: 560.103 secs

Sequence Sequence Sequence Sequence

Sequence Sequence Sequence Sequence

Sequence Sequence

Sequence Sequence Sequence

Sequence Sequence

Sequence

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COUNTRY: USA

ZIP: 22313-0299

COMPUTER READABLE FORM:
MEDIUM TYPE: Rioppy disk
COMPUTER: IBM PC COMPATIble
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                       Sequence 14, Application US/08232463
Fatent No. 5570367
GENERAL INFORMATION:
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
PCT-US93-06251-51
US-08-989-251-28
US-09-340-250-28
US-09-528-108-28
US-09-528-108-28
US-09-593-711A-10
US-09-007-005-17
US-08-770-379-16
US-08-770-379-16
US-09-230-371A-16
US-09-230-371A-10
US-09-25-264-12
US-09-280-173A-10
                                                                                                                                  US-09-018-635-36
US-08-770-379-16
US-08-757-669A-16
US-09-230-371A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
PPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY-AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKT NUMBER: 39472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 72.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
  11192
13320
13320
1320
1320
289
289
289
801
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1357
801
801
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US-08-232-463-14
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   44444444444444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                     CITY: Ale
STATE: VA
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   Query.Match
   Sequence 1, Appli
atent No. 5196516
Sequence 7, Appli
                                                                 March 30, 2003, 09:12:13; Search time 33.7247 Seconds (without alignments) 9093.534 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                              1 gtccttgggtagcatgtaca.....acatgccgcctctccttc 1000
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Sequence 12,
Sequence 8, A
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Sequence
Sequence
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       GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                            -08-770-379-20
-08-757-669A-20
                                                                                                                                                                                                  hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S-09-165-264-11
S-09-165-264-13
S-09-165-264-13
S-09-165-264-8
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-08-726-214-1
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.08-658-136-1
                                                                                                                                                                               441362 seqs, 153338381 residues
                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                               - nucleic search, using sw model
                                                                                                          US-09-691-220-3_COPY_1_1000
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                                                                                                                                                  IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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32207
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                                                                                                          Title:
Perfect score:
                                                                                                                                                  Scoring table:
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47.8
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                                                                                                                              Sequence:
                                                                                                                                                                                Searched:
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                                                                   Run on:
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Length 7218;

DB 1;

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35473 CCCTCATCCCCCTCTCTCTCTCCTCCTCCCCTCTCTCTTCCTTCCTTCTTCTTCCTC 35532
                        945 CCTCCCCCTTCCCAGGCTGCCCCCACTTGCCTGTCCACATGCCGCCTCTCCCTCTC 1000
                                                                                                                                                                                                                                LANDES, GREGORY M
BURN, TIMOTHY C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                            ONE MOUNTAIN ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 508-872-5415
INFORMATION FOR SEQ ID NO: 1:
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Best Local Similarity 58.55
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                      MASSACHUSETTS: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                           FRAMINGHAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                       GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                             US-08-658-136-1
                                                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
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                                                                                                                                                         886 CCTCTGTACTCTGTACTCCTCATCTGGAGCCTTTCCCCCCTTCCTGCTTCTCCTCTCT 945
                                                                                                   826 GCCCGCCCCTCTTCCGTCCTTGTCCCTCGCAGCCCCCTCCTCCTCCTGTACTCGGCGTC 885
                                              GCCAGGGACTGACCAAACCTTGGGGGAGCCTGGGAGCCGGAACTGGTACAAGGGGAGGAC 825
                       Gaps
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                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/658,136
     Pred. No. 7.2e-09;
2; Mismatches 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 59.2; DB 3;
Pred. No. 2.8e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: GEN4-17.8 TELECOMMUNICATION INFORMATION: TELEPHONE: 508-872-8400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSEE: GENZYME CORPORATION
P: ONE MOUNTAIN ROAD
FRAMINGHAM
                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08658136 Patent No. 6071717 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                            KLINGER, KATHERINE W
                                                                                                                                                                                                                                                                                                                                                                        LANDES, GREGORY M
BURN, TIMOTHY C
CONNORS, TIMOTHY D
DACKOWSKI, WILLIAM
GERMINO, GREGORY
Best Local Similarity 11.5%; Pr. Matches 27; Conservative 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 31,845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 508-872-5415
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53526 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: LASSEN, ELIZABETH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: MASSACHUSETTS
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                              GERMINO, GRI
QIAN, FENG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
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APPLICANT:
APPLICANT:
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APPLICANT:
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                                                                                                                                                                      TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE NUMBER OF SEQUENCES: 58
                                                                                                                                                                                                                                                                                                                                                                                           PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.8e-05;
thes 73;
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Pred. No. 2.8e
0; Mismatches
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APPLICATION NUMBER: US/08/658,136
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                             PC-DOS/MS-DOS
                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: GENZYME CORPORATION
Sequence 1, Application US/08658136
Patent No. 6071717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: LASSEN, ELIZABETH
REGISTRATION NUMBER: 31,845
REFERENCE/DOCKET NUMBER: GEN4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 508-872-8400
                                                                                                  CONNORS, TIMOTHY D
DACKOWSKI, WILLIAM
GERMINO, GREGORY
QIAN, FENG
                                                 KLINGER, KATHERINE
                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
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4.9%; Score 49.2;
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Best Local Similarity
Matches 142; Conserv
                           997 TCTC 1000
                                                                                               RESULT 6
US-09-165-264-14/c
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                                                      18 CCCC 15
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Pred. No. 0.0013;
0; Mismatches 159; Indels
                                                                                                                                                                                            Score 51.6; DB 6; Length 4
Pred. No. 0.001;
0; Mismatches 79; Indels
                                 APPLICANT: SCHREURS, CHRISTA S.; METTENLEITER, THOMAS C. DN, ARTUR J.; LUKAS, NOEMI; RZIHA, HANNS J. TITLE OF INVENTION: PSEUDORABIES VIRUS VACCINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Vinayagamoorthy, Thuralayah
TITLE OF INVENTION: Multi-Loci Genomic Analysis
FILE REFERENCE: 44747
CURRENT APPLICATION NUMBER: US/09/165,264
CURRENT FILING DATE: 1998-10-01
NUMBER: OF SEQ ID NOS: 14
SOPTWARE: Patentin Ver. 2.1
                                                                            NUMBER OF SEQUENCES: 8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/383,833
FILLING DATE: 21-JUL-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/09165264
Patent No. 6197510
                                                                                                                                                                                        Query Match 5.2%;
Best Local Similarity 55.6%;
Matches 99; Conservative
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Best Local Similarity 47.7%;
Matches 145; Conservative (
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                     ;Patent No. 5196516
                                                                                                                                      LENGTH: 4897
5196516-7
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LENGTH: 320
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GGCCCGCCCCTCTTCCGTCCTTGTCCCCTCGCAGCCCCCTCTCTCCCTGTACTCGGCGT 884
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Patent NO. 6197510
GENERAL INFORMATION:
APPLICANT: Vinayagamoorthy, Thuraiayah
TITLE OF INVENTION: Multi-Loci Genomic Analysis
FILLE REFERENCE: 44747
CURRENT APPLICATION NUMBER: US/09/165,264
CURRENT FILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO: 12
Sequence 14, Application US/09165264
Patent No. 6197510
GENERAL INFORMATION:
APPLICANT: Vinayammoorthy, Thuraiayah
TITLE OF INVENTION: Multi-Loci Genomic Analysis
FILE REFERENCE: 44747
                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/165,264
CURRENT FILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
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SEQ ID NO 14
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Length 318

DB 4;

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GENERAL INFORMATION:
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US-09-165-264-8
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0; Mismatches 153; Indels
                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Vinayagamoorthy, Thuratayah
TITLE OF INVENTION: Multi-Loci Genomic Analysis
FILE REFERENCE: 44747
CURRENT APPLICATION NUMBER: US/09/165,264
CURRENT FILING DATE: 1998-10-01
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 8
LENGTH: 319
                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/09165264
Patent No. 6197510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08726214; Patent No. 6107076
 nilarity 48.0%;
Conservative
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Best Local Similarity
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            Matches 141;
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452 ACTIGGCCCCGCGCGACCCGGCCCTACGCCTCCTGCC--GCCGCTCTCCGCGTCTCCGGG 509
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Patent No. 6117654
ENERAL INFORMATION:
APPLICAMT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/09/128,155
ENRIENT FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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Pred. No. 0.0053;
0; Mismatches 74; Indels
                                                  MAMMALIAN ADENYLYL CYCLASE
                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICANT: Tang, Wei-Jen
APPLICANT: Gilman, Alfred G.
TITLE OF INVENTION: SOLUBLE MAMMALIAN
TITLE OF INVENTION: AND USES THEREFOR
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: ANDOId, White & Durkee
STREET: P.O. Box 4433
                                                                   AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,214
FILING DATE: Concurrently Herewith
                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/005,498
FILING DATE: 04-OCT-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: UTSD:450
                                                                                                                                                                                                           United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.9%;
58.0%;
                                                                                                                                                                                                                                                                      Floppy disk
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869 TCCCTGTACTCGGCGTCCCTCTGTACTCTGTACTCCTCATCTGGAGCCTTTCCCCCTT 928
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                                                                                               CCCTTCCCAGGCTGCCCCACTTGCCTGTCCACATGCCGCCTCTCCTCTT 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 4.8%; Score 47.8; DB 4; Length 3 Best Local Similarity 47.8%; Pred. No. 0.0038; Matches 139; Conservative 0; Mismatches 152; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 13, Application US/09165264

Patent No. 6197510

GENERAL INFORMATION:
APPLICAR: Vinayagemoorthy, Thuraiayah

TITLE OF INVENTION: Multi-Loci Genomic Analysis

FILE REFERENCE: 44747

CURRENT APPLICATION NUMBER: US/09/165, 264

CURRENT FILING DATE: 1998-10-01

NUMBER OF SEQ ID NOS: 14

SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Vinayagamoorthy, Thuratayah TITLE OF INVENTION: Multi-Loci Genomic Analysis FILE REFERENCE: 44747
CURRENT APPLICATION NUMBER: US/09/165,264
CURRENT FILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 13
LENGTH: 320
                                                                                                                                                                                                                                                                                                                                     Sequence 13, Application US/09165264 Patent No. 6197510 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
                                                                                                                                                                                                          989 CCTCTCCTCTC 1000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      749 CACCACGCCTTCGCTCGGCCAGGGACTGACCATGGGGGAGCCTGGGAGCCGGAAC 808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            809 TGGTACAAGGGAGGACGCCCCCCCTCTTCCGTCCTTGTCCCCTCGCAGCCCCCTCCTC 868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:

CHER INFORMATION: Description of Artificial Sequence: Primer sequence

US-09-165-264-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                         576 GTGATGTCACGGGCAGCGGTGGGTCACTCGGAGGTGAGGCGCCCCCCAGGCGAGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3;
                                                                                                                                                                                                                                                                              Length 152331;
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                                                                                                                                                                                                                                                                                                                  0; Mismatches 122; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 11, Application US/09165264
Retent NO. 6197510
GENERAL INFORMATION:
APPLICANT: Vinayagamoorthy, Thuratayah
TITLE OF INVENTION: Multi-Loci Genomic Analysis
FILE REFERENCE: 4474ABER: US/09/165,264
CURRENT FILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 11
                                                                                                                                                                                                                                                                            4.8%; Score 48.4; DB 3; 51.7%; Pred. No. 0.018;
EARLIER FILING DATE: 1998-07-02
EARLIER APPLICATION NUMBER: US 60/054,646
EARLIER FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                   COCATION: (1)...(152331)
COTHER INFORMATION: n = A,T,C or US-09-128-155-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21902 GGGGGGGGGGGGGGG 21884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   696 TTAAGGGGAGGACACCGGG 714
                                                                                                                                                                                                                                                                         Query Match 4.8%
Best Local Similarity 51.7%
Matches 134; Conservative
                                                                                                                             TYPE: DNA
ORGANISM: Homo saptens
                                                                                                                                                                              NAME/KEY: misc_feature
                                                                                        SEQ ID NO 16
LENGTH: 152331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
US-09-165-264-11/c
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                                                                                                                                                                                                                                                                                                                                                              507 GGGGAAGTGGCCCGGTTCGGCCGGGCAGGGGGCTGGCGGGGGAGCCCCGCGGGGGGGT 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      567 GGCGAGCGGGTGATGTCACGGGCAGCGGTGGGTGGGTCACTCGGAGGTGAGGCGCCGCCA 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       627 GGCGAGTTCAGCGAGAGTTCAGCCGCATTAGCCAAATGAGGCCCGGCCTGGGTGG 686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                  ; OTHER INFORMATION: Description of Artificial Sequence:Primer sequence US-09-165-264-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Primer sequence
US-09-165-264-8
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4.4%; Score 43.8; DB 4; Length 319;
Best Local Similarity 50.2%; Pred. No. 0.037;
Matches 108; Conservative 0; Mismatches 107; Indels
                                                                                                                                    Score 44; DB 4; Length 320;
Pred. No. 0.033;
0; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8, Application US/09165264
Patent No. 6197510
GENERAL INFORMATION:
APPLICANT: Vinayagamoorthy, Thuralayah
TITLE OF INVENTION: Multi-Loci Genomic Analysis
FILE REFERENCE: 44747
CURRENT FILING DATE: 1998-10-01
NUMBER OF SEO ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            687 GGGTGTGTTAAGGGGAGGACACCGGGACCACCC 721
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US-08-770-379-20/c
: Sequence 20, Application US/08770379
                                    TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                      Query Match
Best Local Similarity 50.5%;
Matches 107; Conservative
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SEQ ID NO 13
LENGTH: 320
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US-09-165-264-8
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                                                                   FEATURE:
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                                                  APPLICANT: Edelman, Isidore S.
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: POLYPEPTIDES FROM KAPOSI'S SARCOMA-ASSOCIATED
TITLE OF INVENTION: HERESVIRUS, DNA ENCODING SAME AND USES THEREOF
NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            825 GCCCGCCCCTCTTCCGTCCTTGTCCCTCGCAGCCCCCTCTCTCCCTGTACTCGGCGT 884
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                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.3%; Score 43.2; DB 2; 52.8%; Pred. No. 0.22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                               1: Cooper & Dunham LLP
1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              March 30, 2003, 13:54:01
                                                                                                                                                                                                                                                                                                                                                                                                                          US/08/770,379
                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 391-0525
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA~(genomic)
Chang, Yuan
Bohenzky, Roy A.
Russo, James J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 32207 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best_Local Similarity 52.8
Matches 93; Conservative
                                                                                                                                      NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
                                                                                                                                                                                                                                              10036
10036
                                                                                                                                                                                                                       New York
: New York
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Job time: 239.725 secs
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                                                                                                                                                                                  ADDRESSEE:
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                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                            STATE:
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March 30, 2003, 13:12:08; Search time 75.6932 Seconds (without alignments) 11242.392 Million cell updates/sec
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GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                         US-09-691-220-3_COPY_1_1000
                                                                                  OM nucleic - nucleic search, using sw model
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                                                                                                                                                                                                                                            1000
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0
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Total number of hits satisfying chosen parameters:

574371 seqs, 425486471 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

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/cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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/cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:* /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:* /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:* /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:* /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:* /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*/cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*/cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*/cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*/ Published_Applications_NA:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Sequence 33, Appl Sequence 29, Appl Sequence 47, Appl Sequence 8, Appl Sequence 202, App Sequence 292, App Sequence 529, App Sequence 529, App Sequence 16, Appl Sequence 20, Appl Sequence 48, Appl Sequence 48, Appl Sequence 48, Appl Sequence 47, Appl Sequence 8, Appl Sequence 20, Appl Sequence 16, Appl Sequence 202, App Sequence 1, Appl: Description US-10-032-393-47 US-10-032-393-8 US-10-184-644-202 US-09-954-456-292 US-09-954-456-529 US-09-954-456-529 US-09-971-10-16 US-09-771-208-20 US-09-771-208-20 US-10-032-393-47 US-10-032-393-8 US-09-804-682-20 US-10-023-529-48 US-10-023-523-48 Query Match Length DB 440 43058 43058 43058 152331 659158 12733 152331 4 8 8 4 4 8 8 4 4 8 6 4 4 7 4 7 4 Score 48.4 Result . Я

e e 9997, 8 46, A	Sequence 210, App Sequence 210, App
	US-10-01/-08LA-210 US-09-978-824-210
6 6 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	0 0 0
936 836 1062 2307 2307 2307 671 950 950 950 173808 173808 173808 3716 3716 3716 3716 3716 3716 3716	3716
	4.4
4.08.88.444.444.444.444.444.444.444.444.	41.2
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0 000	

ALIGNMENTS

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GENERAL INFORMATION

APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
APPLICANT: GERMINO, Gregory
APPLICANT: GERMINO, Gregory
APPLICANT: PHE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
APPLICANT: PHAKDEEKITCHAROEN, Bunyong
ITILE OF INVENTION: DETECTION AND TREATMENT OF POLYCYSTIC KIDNEY DISEASE
FILE REFERENCE: JH01680-2
CURRENT APPLICATION NUMBER: US/09/904,968A
CURRENT APPLICATION NUMBER: US 60/283,691
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2000-07-13
NUMBER OF SEQ ID NOS: 113
SOFTWARE PATENTIN VERSION 3.0
SEQ ID NO 1
LENGTH: 53522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     825 CGCCCCCCCTCTTCCGTCCTTGTCCCCTCGCAGCCCCCTCCTCTCCCTGTACTCGGCGT 884
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RESULT 1
US-09-904-968A-1
Sequence 1, Application US/09904968A
; Publication No. US20030008288A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-904-968A-1
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FILE REFERENCE: 130001.406
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CCCATION: 14, 21, 27, 33, 36, 42, 72, 101, 103, 207, 208, 221, 223, 10CATION: 227, 235, 240, 242, 243, 247, 248, 259, 263, 269, 273, 278, 10CATION: 226, 321, 322, 324, 330, 332, 335, 336, 340, 367, 371, 385, 10CATION: 390, 393, 394, 401, 407, 415, 421, 447, 454, 471, 475, 0THER INFORMATION: n = A,T,C or G

NAME/KEY: misc_feature

LOCATION: 479, 494, 501, 508, 511, 513, 525, 539, 540, 579, 596, 605, 10CATION: 623, 624, 633, 654, 656, 658, 664, 670, 679, 711, 713, 10CATION: 798, 802, 808, 810, 813, 814, 820, 822, 824, 825, 838

NAME/KEY: misc_feature

LOCATION: 978, 1002, 1008, 1029, 1034, 1057, 1065

UCCATION: 973, 1002, 1005, 1028, 1029, 1034, 1057, 1065
                                                                                                                APPLICANT: Corey, Michael J.

APPLICANT: Corey, Michael J.

TITLE OF INVENTION: PAL-18 POLYPEPTIDES, NUCLEIC ACIDS

TITLE OF INVENTION: ENCODING THE SAME AND METHODS FOR SCREENING FOR OR.

TITLE OF INVENTION: MODULATING THE SAME

FILE REFERENCE: 130001.406

CURRENT APPLICATION NUMBER: US/09/804,682

CURRENT FILING DATE: 2001-03-12

NUMBER OF SEQ ID NOS: 174

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 29, Application US/09804682
Patent No. US20020106765A1
GENERAL INFORMATION:
APPLICANT: Kinders, Michael J.
APPLICANT: Corey, Michael J.
TITLE OF INVENTION: PAL-18 POLYPEPTIDES, NUCLEIC ACIDS
TITLE OF INVENTION: PROCEDING THE SAME AND METHODS FOR SCREENING FOR OR
TITLE OF INVENTION: MODULATING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              716 CCACCCCCTCTTCCCCGCCCCACCACCTCCTCCACGGCTTCGCTCGGCCAGGGACT 775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 836 CTTCCGTCCTTGTCCCCTCGCAGCCCCCTCTCCCCTGTACTCGGCGTCCCTCTGTACT 895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    896 CTGTGTACTCCTCATCTGGAGCCTTTCCCCCTTCCTGCTTCTCCTCCTCCTCCTCCCCTTC 955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1065;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 5.4%; Score 54.4; DB 10; Length Best Local Similarity 45.6%; Pred. No. 6.6e-06; Matches 130; Conservative 0; Mismatches 155; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      956 CCAGGCTGCCCCCACTTGCCTGTCCACATGCCGCCTCTCCCTCTC 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         645 CCCCCTINNCNCNCCCTCNCCCCCNCCTTCCCANCCCTCCTCC 689
                                             Sequence 33, Application US/09804682 Patent No. US20020106765A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
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Publication No. US20030027286A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Haselbeck, Robert
APPLICANT: GTOSS, MOLLY
TILE OF INVENTION: BACTERIAL PROMOTERS AND METHODS OF USE
FILE REFERENCE: ELITRA 010A;
CURRENT APLICATION NUMBER: US/10/032,393
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/248,993
PRIOR APPLICATION NUMBER: 09/248,993
PRIOR FILING DATE: 2001-09-06
PRIOR FILING DATE: 2001-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
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                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: 5, 6, 16, 21, 24, 25, 33, 39, 72
LOCATION: 325, 237, 238, 244, 245, 246, 25
LOCATION: 321, 323, 334, 344, 455, 45
LOCATION: 397, 405, 432, 437, 454, 455, 45
COTHER INFORMATION: n = A,T,C or G
NAME/KEY: misc_feature
LOCATION: 485, 487, 488, 494, 496, 499, 51
LOCATION: 583, 600, 611, 613, 623, 624, 65
CURRENT APPLICATION NUMBER: US/09/804,682
CURRENT FILING DATE: 2001-03-12.
NUMBER OF SEQ ID NOS: 174
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 858, 878, 884, 886, 896, 897, 10CATION: 957, 961, 965, 981, 991, 993, 10CATION: 1043, 1047, 1049, 1051, 1054, US-09-804-682-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 485, 487, 488, 494, 496, LOCATION: 583, 600, 611, 613, 623, LOCATION: 694, 701, 713, 716, 720, LOCATION: 744, 781, 782, 785, 789, OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 44.0
Matches 129; Conservative
                                                                                                                                                                            TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
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                                                                                                                                                                                                                                                                                                        910 TCTGGAGCCTTTCCCCCCTTCCTGCTTCTCCTCCTCCCCCCTTCCCAGGCTGCCCCCA 969
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                                                                                                                                                             Gaps
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                                                                                                                           Length 12733;
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Publication No. US20030027286A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Wall, Daniel
APPLICANT: Gross, Molly
TITLE OF INVENTION: BACTERIAL PROMOTERS AND METHODS OF USE
FILE REFERENCE: ELITRA.010A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 5.1%; Score 51; DB 9; Length 127 Best Local Similarity 47.1%; Pred. No. 8.7e-05; Matches 156; Conservative 0; Mismatches 175; Indels
                                                                                                                                                          0; Mismatches 175; Indels
                                                                                                                              Score 51; DB 9;
Pred. No. 8.7e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/032,393
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 60/259,434
PRIOR FILING DATE: 2000-12-27
PRIOR APPLICATION NUMBER: 09/948,993
PRIOR FILING DATE: 2001-09-06
PRIOR PILING DATE: 2001-09-06
PRIOR FILING DATE: 2000-09-06
NUMBER OF SEQ ID NOS: 68
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    970 CTTGCCTGTCCACATGCCGCCTCTCCTCTC 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                  ; OTHER INFORMATION: Vector peper14
US-10-032-393-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ); OTHER INFORMATION: Vector pEPEF1
US-10-032-393-8
                                                                                                                             5.1%;
                                       TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                                                          Best_Local Similarity 47.19
Matches 156; Conservative
          SEQ ID NO 47
LENGTH: 12733
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US-10-032-393-8/c
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LENGTH: 12739
                                                                                                                              Query Match
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                                                                      FEATURE:
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APPLICANT: Chen, Jian
APPLICANT: Chen, Jian
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Applicant: Shang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERBNCE: P3430R1C227
CURRENT APPLICATION NUMBER: US/10/184, 644
                            730 CCCGCCCCACCACCTCCTCCACCACGCTTCGCTCGGCCAGGGACTGACCAAACCTTGGG 789
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HGADAVRGSWQGVPGHSGAWETSGGHGIFGSQGGLGGQGGGNPGGLGTPWVHGYPGNSAG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           324 AGCACCCGCCGCGCGCGCGCGCGCGCGCCGGAGTCACATGATGTCACAGACAA 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          384 TGACACAAGCCGGTGTCTCATTCCGACACAGCGTCCGAGCTGCACAATGTCACACCCGGG 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              444 TGCCAAACACTTGGCCCCGCGGGCCCGGCCCTACGCCTCCTGCCGCCGCTCTCCCGCGTC 503
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                                                                                                                                   SFGMNPQGAPWGQGGNGGPPNFGTNTQGAVAQPGYGSVRASNQNEGCTNPPPSGSGGGSS
                                                                                                                                                                                850 CCCTCGCAGCCCCCTCTCCCTGTACTCGGCGTCCCTCTGTACTCTGTGTACTCCTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.8%; Score 48.4; DB 9;
18.2%; Pred. No. 0.00028;
iive 93; Mismatches 185;
                                                                                                                                                                                                                                                                                                                                                                                                     970 CITGCCIGICCACAIGCCGCCICICCCTCTC 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 202, Application US/10184644; Publication No. US20030044930A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Baker, Kevin P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Homo Sapien
US-10-184-644-202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-184-644-202
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LENGTH: 440
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Best Local S
Matches 62
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sequence 249, Application US/09954456
Fatefit No. US20020115057A1
GENERAL INFORMATION:
TOUR SELECTION SELS
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using
TITLE OF INVENTION: Sets
TITLE OF INVENTION: Sets
TITLE OF INVENTION: Sets
CURRENT PEPLICATION NUMBER: US/09/954,456
CURRENT PELING DATE: 2000-09-18
FRIOR PELING DATE: 2000-09-18
FRIOR PELING DATE: 2000-09-25
FRIOR APPLICATION NUMBER: US/60/234,923
FRIOR APPLICATION NUMBER: US/60/234,923
FRIOR APPLICATION NUMBER: US/60/235,134
FRIOR PELING DATE: 2000-09-26
FRIOR APPLICATION NUMBER: US/60/235,637
FRIOR PELING DATE: 2000-09-26
FRIOR PELING DATE: 2000-09-27
FRIOR APPLICATION NUMBER: US/60/235,711
FRIOR APPLICATION NUMBER: US/60/235,712
FRIOR APPLICATION NUMBER: US/60/235,720
FRIOR PELING DATE: 2000-09-27
FRIOR FILING DATE: 2000-09-27
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; Pred. No. 0.00056;
. 0; Mismatches 116; Indels 2;
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APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer FILE REFERENCE: 44921-5028-WO
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Patent No. US20020142981A1
GENERAL INFORMATION:
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Matches 130; Conservative
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TITLE OF INVENTION: Pacess for Identifying Anti-Cancer Therapeutic Agents Using Canc
TITLE OF INVENTION: Sets
FILE REPERENCE: 689290-76
CURRENT APPLICATION NUMBER: US/60/234,615
CURRENT FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US/60/234,052
PRIOR APPLICATION NUMBER: US/60/234,052
PRIOR APPLICATION NUMBER: US/60/234,923
PRIOR PILING DATE: 2000-09-20
PRIOR PILING DATE: 2000-09-25
PRIOR PELING DATE: 2000-09-25
PRIOR PELING DATE: 2000-09-25
PRIOR PELING DATE: 2000-09-26
PRIOR PELING DATE: 2000-09-27
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Pred. No. 0.00056;
0; Mismatches 116; Indels
                                                                                                                EISKEGNRLLGGSGDNYRGQGSSWGSGGGDAVGGVNTVNS 402
                                                                    624 CCAGGCGAGTTCAGCGAGAGTTCAGCCGCATTGCATTAGG 663
                                                                                                                                                                                                                                                                                                 Sequence 292, Application US/09954456
Patent No. US20020115057A1
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SOFTWARE: PatentIn version 3:0
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Best Local Similarity 52.4%;
Matches 130; Conservative
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; ORGANISM: Homo sapiens
US-09-954-456-292
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LENGTH: 43058
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US-09-954-456-529
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GENERAL INFORMATION:
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LENGTH: 659158
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Sequence 16, Application US/10095407

Patent No. US20020164330A1

GENERAL INFORMATION:
APPLICANT: Pan, Yang

TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY

TITLE OF INVENTION: AND USES THEREOF

FILE REFERENCE: 0940/4052001

CURRENT APPLICATION NUMBER: US/10/095,407

CURRENT FILING DATE: 2002-03-11
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FERTURE:
CATHER INFORMATION: Genbank Accession No. US20020142981A1 284721
US-09-880-107-3950
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Best Local Similarity 52.4%; Pred. No. 0.00056;
Matches 130; Conservative 0; Mismatches 116;
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4.8%; Score 48.4; DB 9;
Best Local Similarity 51.7%; Pred. No. 0.00068;
Matches 134; Conservative 0; Mismatches 122;
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PRIOR FILING DATE: 1998-07-02
PRIOR FILING DATE: 1998-07-02
PRIOR FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 3.0
SSOFTWARE: 152331
                CURRENT FILING DATE: 2001-06-7/
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR PEPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFUMARE: PATENTIN VET. 2.1
SEQ ID NO 3950
LENGTH: 43058
CURRENT APPLICATION NUMBER: US/09/880,107
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LCCATION: (1)...(152331)

COTHER INFORMATION: n = A,T,C or G

US-10-095-407-16
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576 GTGAIGTCACGGGCAGCGGIGGGTGACTCGGAGGIGAGGCGCCCCCCAGGCGAGTTC
                                                                             APPLICANT: BRADFORD, ERIC
APPLICANT: HORVAT, SIMON
TITLE OF INVENTION: CLONING OF A HIGH-GROWTH GENE
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OTHER INFORMATION: n is unidentified a, c, g,
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CURRENT APPLICATION NUMBER: US/09/771,208
CURRENT FILING DATE: 2001-01-26
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LOCATION: (546998)..(547017)
OTHER INFORMATION: n is unidentified a,
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LOCATION: (346860)..(346823)
OTHER INFORMATION: n is unidentified a,
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LOCATION: (317174)..(317193)
OTHER INFORMATION: n is unidentified a,
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PRIOR FILING DATE: 1997-12-29
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.0
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OTHER INFORMATION: n is unidentified NAME/KEY: misc._feature.
LOCATION: (602466)..(602485)
OTHER INFORMATION: n is unidentified
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LOCATION: (494715)...(494814)
OTHER INFORMATION: n is unidentified
NAME/KEY: misc_feature
LOCATION: (390986)...(391005)
OTHER INFORMATION: n is unidentified
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LOCATION: (271829) ..(271848)
OTHER INFORMATION: n is unidentified
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LOCATION: (280353)..(280373)
OTHER INFORMATION: n is unidentified
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                                                                                                                                                         696 TTAAGGGGAGGACACCGGG 714
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LOCATION: (170625)..(170645)
                                                                                                                                                                                                                                                                                                                                                              JUAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
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735 GCGAGGGGGGGCCTGTGGCGGCACGGCGGCGGCGCCGCGGGGGGGCGCCCGGGCCGGGGG 676
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Patent No. US20020152485A1
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
                                                                                                                                                                                             Sequence 48, Application US/10023529
Patent No. US20020123388A1
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Oryctolagus cuniculus
                                                                                        675 ceccececececes 655
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Matches 110; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) NAME/KEY: CDS
; LOCATION: (246)...(1895)
US-10-023-529-48
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APPLICANT: Lees, Ann M.
APPLICANT: Lees, Nobert S.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: RYPERSOLIES AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: APPERSOLIES 10797-004001
TITLE OF INVENTION: APPERSOLIES 10797-004001
FILE REFERENCE: 10797-004001
CURRENT FILING DATE: 2000-01-10-12
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR PLILING DATE: 1997-11-26
PRIOR PLILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR PLILING DATE: 1997-11-27
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR PLILING DATE: 1997-11-27
PRIOR PLILING DATE: 1997-11-27
PRIOR PLILING DATE: 1997-10-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                 885 CCCTCTGTACTCTGTACTCCTCATCTGGAGCCTTTCCCCCTTCCTGCTTCTCCTCTT 944
                                                                                                                                                                                                                                                    825 CGCCCCCCCTCTTCCGTCCTTGTCCCCTCGCAGCCCCCTCCTCTCCCTGTACTCGGCGT 884
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                                                                                                                                                                    Query Match 4.8%; Score 48; DB 9; Length 659158; Best Local Similarity 54.5%; Pred. No. 0.0011; Matches 96; Conservative 0; Mismatches 80; Indels 0
                                                                                                                                                                                                                 80; Indels
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      or
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Pred. No. 0.0032;
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                 NAME/KEY: misc_feature
| LOCATION: (132680)...(132700)
| OTHER INFORMATION: n is unidentified a,
| NAME/KEY: misc_feature
| OTHER INFORMATION: n is a, c, g, or t
US-09-771-208-20
OTHER INFORMATION: n is unidentified
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Best Local Similarity 54.7%;
Matches 110; Conservative
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SEQ ID NO 48
LENGTH: 2561
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565 CIGGCGAGCGGGTGATGTCACGGGCAGCGGTGGGTGGGTCACTCGGAGGTGAGGCGCCGC 624
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 2561;
APPLICANT: Lees, Ann. W.
APPLICANT: Lees, Shoert S.
APPLICANT: Lees, Shoert S.
APPLICANT: Law, Shoon W.
APPLICANT: Law, Shoon W.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/10/23,529
CURRENT APPLICATION NUMBER: 09/616,289
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-02
PRIOR FILING DATE: 1997-11-26
PRIOR FILING DATE: 1997-11-27
PRIOR FILING DATE: 1997-11-27
PRIOR FILING DATE: 1997-11-27
PRIOR FILING DATE: 1997-11-27
PRIOR FILING DATE: 1997-10-36
NUMBER OF SEQ ID NOSE: 53
SOSTWARE: FASTSEQ FOR WINDOWS VERSION 4.0
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Pred. No. 0.0032;
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54.7%; Pred. No. v...
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 2561;
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Publication No. US20030027286A1
GENERAL INFORMATION:
APPLICANT: Haselbock, Robert
APPLICANT: Wall, Daniel
APPLICANT: Wall, Daniel
APPLICANT: Wall, Daniel
APPLICANT: Wally
TITLE OF INVENTION: BACTERIAL PROMOTERS AND METHODS OF USE
FILE REFERENCE: ELITENA.0104
CURRENT APPLICATION NUMBER: US/10/032,393
CURRENT FILING DATE: 2001-12-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.5%; Score 45; DB 12;
nllarity 54.7%; Pred. No. 0.0032;
Conservative 0; Mismatches 90
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PRIOR FILING DATE: 2000-12-27
PRIOR FILING DATE: 2001-09-06
PRIOR FILING DATE: 2001-09-06
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
NUMBER OF SEQ ID NOS: 68
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 47
LENGTH: 12733
                                                                                                                         PRIOR APPLICATION NUMBER: US/09/616,289
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-03-02
PRIOR PILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR PILING DATE: 1997-11-26
PRIOR PILING DATE: 1997-11-27
PRIOR PILING DATE: 1997-11-27
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FASTSEQ for Windows Version 4.0
SSOFTWARE: 2561
                                                                                     CURRENT APPLICATION NUMBER: US/10/023,523 CURRENT FILING DATE: 2001-12-17
                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Oryctolagus cuniculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGCCGCGCGCGACGGGCG 655
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; NAME/KEY: CDS
; LOCATION: (246)...(1895)
US-10-023-523-48
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Best Local Similarity
Matches 110; Conserva
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5324 GGGGGGGGGGGGGGGGGGGGGGGTCGACCGATGCCCTTGAGAGCCTTCAACCCAGTCA 5383
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                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                687 GGGTGTGTGTTAAGGGGAGGACACCGGGACCACCCCCCTCTTCCCCGCCCCCACCACCTCC
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                                                                 Length 12733;
                                                               Score 45; DB 9; Length 127
Pred. No. 0.0042;
0; Mismatches 140; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 747 TCCACCACGGCTTCGCTCGGCCAGGGACT 775
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ne : 956.693 secs
; OTHER INFORMATION: Vector pEPEF14 US-10-032-393-47
                                                                   4.5%;
                                                                                      Best Local Similarity 48.0
Matches 129; Conservative
                                                                       Query Match
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UI-E-EJO-603045668

BF061934 7k69c04.x BM849644 K-EST0129

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929 bp mRNA linear EST 15-JUL-2002 5', mRNA sequence. B0678320 IG:21790999
                                                                                                                                                                                                                       A1269913 qk04e00.x
A1995003 wn26h01.x
A178478 wn22d05.x
A137049 qx82f05.x
A141453 tf15c02.x
A141453 tf15c02.x
A1458982 tf15c02.x
A1458982 tf15c02.x
A1458982 tf15c02.x
A1458982 tf15c02.x
A145986 yv42a08.s1
N54985 yv42a08.s1
A1503919 cv67d09.s
A124348 qh30f09.s
A1243348 qh30f09.x
A136408 nc58109.x
A1040836 cx27f05.s
BM922787 AGENCOURT
                   BI759786 603045668
BQ011927 UI-1-BC1p
AW139412 UI-H-BI1-
BM681212 UI-E-EJ0-
                                                                         AA404273 zv63d08.s
BF435919 nab33e01.
AI478236 tm50903.x
BE857582 7903e12.x
BE857345 7928c05.x
                                                                                                                         A1627663 ty81d04.x
A1636506 ts91b08.x
BF002162 7h23c02.x
BQ013411 UI-1-BC1p
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AA677219 zj54h09.s
AW138698 UI-H-BI1-
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BE466668 hz23h06.x
A1091348 oo22e09.x
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 929)
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2499 row: 1 column: 04
High quality sequence stop: 564.
I. 929
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                                                                                                                                                                                                                                                                                             N25921
N54985
AI003919
AI243348
AW136405
                            BQ011927
AW139412
BM681212
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A1636506
BF002162
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BE466668
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AW138698
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BF594423
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AI040836
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AI421453
AI458982
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AI768478
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 Homo sapiens
human.
494.6
485
482
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423.8
422.6
409.6
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317.8
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BQ678320/c
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JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
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KEYWORDS
SOURCE
(without alignments)
12561.622 Million cell updates/sec
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                                                                                                      US-09-691-220-3_COPY_1_1000
1000
1 gtccttgggtagcatgtaca.....acatgccgcctctccctct 1000
                                                               March 30, 2003, 08:06:43; Search time 1289.28 Seconds
                                                                                                                                                                                           32308132
         GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                        of hits satisfying chosen parameters:
                                                                                                                                                                       16154066 seqs, 8097743376 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                             nucleic search, using sw model
                                                                                                                                           IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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em_gss_hum:*
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gb_htc: *
gb_est3: *
gb_est4: *
gb_est5: *
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Post-processing:

Database

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FEATURES

BQ678320 AGENCOURT BM702028 UI-E-CQ1-BM71329 UI-E-EJ0-BM72659 UI-E-EJ0-BM931367 UI-E-EJ1-BM981448 UI-CF-EN1

BQ678320 BM702028 BM713229 BM726559 BM931567 BM981448

929 602 603 591 579 652

590 567.4 563 535 517.6

656.2

Result Š.

Description

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/tissue_Inpe="optic nerve"
/dev_stage="adult"
/lab_host="bluble"
/lab_host="bluble"
/lab_host="bluble"
/note="Organ: ege; vector: pT773-pec (Pharmacia) with a modified polylinker; Site_1: EcoR I: Site_2: Not I;
/note="Organ: ege; vector: pT773-pec (Pharmacia) with a modified polylinker; Site_1: EcoR I: Site_2: Not I;
/ur="cQ1 is a normalized cDNA library containing the following tissue(s): optic nerve: The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oilygo-dr primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT773-pac vector: The oilgonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CCATTAAGTG: This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Figure 1: State St
                                                                                                                                                                                             Eukaryotania Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 602)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
7el: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTITCTTCCAGTGAAACGTGCATCCCGAGGGCTTCTAGGATGAAGTAGTCCACTGGAAGG 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ij
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Program for Rat Gene Discovery and Mapping
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Pred. No. 1.2e-125;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="UI-E-CQ1-aex-p-12-0-UI"
/clone_lib="UI-E-CQ1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .602
/organism-"Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                               Genome Res. 6 (9), 791-806 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .ocation/Qualiflers
                                                                                          BM702028.1 GI:19015286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq primer: M13 Reverse
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99.7%;
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                                                                                                                                                                            Homo sapiens
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Best Local 3
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              DEFINITION
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ORIGIN
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TITLE
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COMMENT
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                                                                   ACCESSION
                                                                                          VERSION
KEYWORDS
SOURCE
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/organisme"Homo sapiens"

/db.ref="taxon::9606"
/clone="INAGE:6294603"
/clone_lb="NIME_MGC_112"
/tissue_type="melanotic melanoma, cell line"
/tasue_type="melanotic melanoma, cell line"
/lab_host="bull0B (phage-resistant)"
/lab_host="bull0B (phage-resistant)"
/note="Organ: skin, Vector: pOTB7; Site_1: xhoI; Site_2:
/note="Organ: skin, Vector: pOTB7; Site_1: xhoI; Site_2:
ECORI: cDNA made by oligo-dT priming. Directionally cloned
into ECORI/ANDI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ij
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  541 TGGCGGGCGAGCCCCGCGGGCGGGCTGGCGGGTGATGTCACGGGCAGCGGTGGTG 600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCCTTTTATCTCTCCAGAGCTGGACAGTGCACCAGGGGCCGGTACTGGTTCCCCCAGCTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             337 GTCACACATGATGACAGACAATGACACAAGCCGGTGTCTCATTCCGACACAGCGTCCG
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Pred. No. 7.5e-141;
0; Mismatches 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 319 335 8250

Fax: 319 335 8250

Fax: 319 335 8250

Exa: 319 335 9565

Exa: 319 336 956

Exa: 319 336 956

Exa: 319 337 9565

Exail: msoares@blue.weeg.uiowa.edu

Tissue Procurement: Dr. Gregg Hageman

CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa

DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa

Clone Distribution: Researchers may obtain clones from Research
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
I (bases 1 to 603)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
                            GGCGGCCGGAGTCACACATGATGTCACAGACAATGACACAAGCCGGTGTCTCATTCCGAC 410
                                                                                                                                                                                                                                                                                                                                        650
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The following repetitive elements were found in this CDNA sequence: 138-191, >(CGGG)n#Simple_repeat (matched compliment) Seq primer: M13 Reverse.
                                                                                                        GGCAGGGGCTGGCGGGCGAGCCCCGCGGGCGGGCTGGCGAGCGGGGTGATGTCACGGGCA 124
483 CCCCAGCTAGGAGACACCTTGGGCGGGCTTTGCTCGCCGGAAGCACGCAGAGCGTGGGG 424
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                                                                                                                                                                                                              GCCAGGGGGCGGGCGGGCCCCCGCGGGCCTGGCCGAGCGGGTGTCACGGGCA
                                                                                                                                                                                                                                                                                                                                     GCGGTGGGTGGGTCACTCGGAGGTGAGGCGCCGCCAGGCGAGTTCAGCGAGAGTTCAGCC
                                                                                                                                                                                                                                                                                                                                                                    GCGGTGGGTGGGTCACTCGGAGGTGAGGCGCCCAGGCGAGTTCAGCGAGAGTTCAGCC
                                                                                                                                                                                                                                                                                                                                                     Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
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97044477
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AUTHORS
TITLE
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/uev_stage="retal and adult"
/uab_host="Maple Life Technologies) (TI phage resistant)"
/uab_host="Maple Life Technologies) (TI phage resistant)"
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UT E-ED0 is a subtracted cDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT7T3-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tags for this library are: fetal eyes, AGAATCAAGA
; lens, CGATTAAGGA; retina, CGGG; Retina Foveal and
Macular, GTCC; RPE and Choroid, ACCTA. This library was
created for the program, Gene Discovery in the Visual
System, supported by National Eye-Institute (NEI)."
/tissue_type="fetal eyes, lens, eye anterior segment, optic nerve, retina, Retina Foveal and Macular, RPE and Choroid"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         173 CCAGCTCTTCCTTTTATCTCTCCCAGAGCTGGACAGTGCACCAGGGGCCGGTACTGGTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     543 CCAGCTCTTCCTTTTATCTCTCCCAGAGCTGGACAGTGCACCACGGGGCCGGTACTGGTTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    363 CGGCCGAAGTCACACATGATGTCACAGACAATGACACAAGCCGGTGTCTCATTCCGACAC
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Pred. No. 1.9e-120;
0; Mismatches 1;
                                                                                         dev_stage-"fetal and adult"
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/nto="Organ: eye; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; UI-E-EJ0 is a subtracted cDNA library constructed
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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/ Organism="Nemoo saplens"

//b.rarf="texton:9606"

/clone="UI-E-EJ0-aii-i-18-0-UI"

/clone="Lib="UI-E-EJ0"

/tissue_type="fetal eyes, lens, eye anterior segment, optic nerve, retina, Retina Foveal and Macular, RPE and
                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 591)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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The following repetitive elements were found in this cDNA
sequence: 132-185, -/CGGG]n#Simple_repeat (matched compliment)
Seq primer: M13 Reverse.
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                                        BM726559 591 bp mRNA linear EST 01-
UI-E-EJO-aii-i-18-0-UI.rl UI-E-EJO Homo sapiens CDNA clone
UI-E-EJO-aii-i-18-0-UI 5', mRNA sequence.
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Best Local Similarity 100.0%; Pred. No. 1.9e-119;
Matches 563; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
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97044477
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AUTHORS
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BM931567 579 bp mRNA linear EST 13-MAR-2002 UI-E-EJ1-ajk-j-22-0-UI.rl UI-E-EJ1 Homo sapiens cDNA clone UI-E-EJ1-ajk-j-22-0-UI 5', mRNA sequence.
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Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                             412
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The following repetitive elements were found in this CDNA sequence: 114-167, 9/CGGG)n#Simple_repeat (matched compliment) Seq primer: M13 REVERSE.
299 CCCCTCTGCCTGTTTGTGCCAACAGCACCGGGGTGCCGCGTCGGGTTCCGGCGGCCG 358
                                                                                                                                                                                                                                                                                                                                                                            291 CGAGCTGCACAATGTCACACCCGGGTGCCAAACACTTGGCCCCGCGGGGGGCCGGGCCTAC 232
                                                                                                                                                                              419 CGAGCTGCACAATGTCACCCGGGTGCCAAACACTTGGCCCCGGGGGGGCCGGGCCTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              239 AGGAGACACCTTGGGCGGGCTTTGCTCGCCGGAAGCACGCAGAGCGTGGGGAGGAGGGC
                                                                                        GAGTCACACATGATGTCACAGACAATGACACAAGCCGGTGTCTCATTCCGACACAGCGTC
                                                                                                                                                                                                                                                                                                                                                                                                                        GCCTCCTGCCGCCGCTCTCCGCGTCTCCGGGGGAGGTGGCCCCGGTTCGGCCCGGGCAGGGG
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Program for Rat Gene Discovery and Mapping
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Cells:
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies) (Tl phage resistant)"
/lab_host="DH10B (Life Technologies) (Tl phage resistant)"
/note="Gran: Lung; Vector: pT73.Pac (Pharmacia) with a
modified polylinker; Site_l: EcoR I; Site_2: Not I;
UI-CF-ENI is a normalized cDNA library containing the
following tissue(s): Primary Lung Cystic Fibrosis
Epithelial Cells. The library was constructed according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was ligated to an EcoR I adaptor, digested with Not
I, and cloned directionally into pT773-Pac vector. The
oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 FORWARD
POLYA=Ves.
                                               EST 21-MAR-2002
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                                                                                                                                                                                                   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases: 1 to 652)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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                                        BM981448 652 bp mRNA linear EST 21-MA UI-CF-ENI-adh-p-17-0-UI.SI UI-CF-ENI Homo sapiens cDNA clone UI-CF-ENI-adh-p-17-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                           University of Iowa 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA Tel: 319 356 4866 Fax: 319 356 7171 Email: paul-mccray@uiowa.edu
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/clone_lib="UI-CF-EN1"
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98.1%; Pred. No. 5.8e-109;
ive 0; Mismatches 10;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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BM981448.1 GI:19603947
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Matches 523; Conservative
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                                                                                                                      /dev_stage="fetal and adult"
//dev_stage="fetal and adult"
//lab_host="DH10B (Life Technologies) (TI phage resistant)"
//note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: ECOR I; Site_2: Not I;
UI-E-EJI is a subtracted cDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dr primer containing a Not I site. Double stranded cDNA was ligated to an ECOR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are: fetal eyes, AGAATCAAGA; lens, CGATTAGCGA; eye anterior segment, AATGCCGAT; optic nerve, CCATTAAGTG; retina, CGGC; Retina Foveal and Macular, GTC; RPE and Choroid, ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3;
                                                           optic nerve, retina, Retina Foveal and Macular, RPE and Choroid"
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Pred. No. 5.5e-113;
0; Mismatches 0;
/db_xref="taxon:9606"
/clone="UI-E-EJ1-ajk-j-22-0-UI"
/clone_lib="UI-E-EJ1"
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Matches 568; Conservative
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61 CCCCTCCTCCAGGGGTATCCCCTCTTTCTAGGGACCTACCCAAGCTAGGCCTTTCTTCCA 120

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Matches 500; Conservative
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451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoareseblue.weeg.ulowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 627), Bonaldo, M.F., Lennon, G. and Soares, M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa Clone Distribution: Researchers may obtain clones from Research Sequetics (www.resgen.com).

Seq primer: M13 Forward

POLYA-Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="fetal eyes, lens, eye anterior segment, optic nerve, retina, Retina Foveal and Macular, RPE and
180 CCCTCCTCCAGGGGTATCCCCTCTTTCTAGGGACCTACCCAAGCTAGGCCTTTCTTCCA 239
                                                      180
                                                                                                               181 TCCTTTTATCTCTCCAGAGCTGGACAGTGCACCAGGGGCCGGTACTGGTTCCCCCAGCTAG 240
                                                                                                                                   300
                                                                                                                                                                                                  421 AGCTGCACAATGTCACACCCGGGTGCCAAACACTTGGCCCCGGGGGGCCCGGCCCTACGC 480
                                                                                                                                                                                                                                                                                                                                                                                                    301 CCTCTGCCTGTGTTTGTGCCAACAGCACCGGCGTGCCGCGTCGGGTTCCGGCGGCGGCGGA 360
                                                                                                                                                                                                                                                                                                                 GTCACACATGATGTCACAGACAATGACAAGCCGGTGTCTCATTCCGACACAGCGTCCG 420
                                                                   BM684023 627 bp mRNA linear EST 27-UI-E-EJ1-ajk-j-22-0-UI.sl UI-E-EJ1 Homo sapiens cDNA clone
UI-E-EJ1-ajk-j-22-0-UI 3', mRNA sequence.
                                                  121 GIGAAACGIGCATCCCGAGGGCTTCTAGGATGAAGTAGTCCACTGGAAGGCACCAGCTCT
                                                                                                                                                                                 241 GAGACACCTTGGGCGGGGCTTTGCTCGCCGGAAGCACGCAGAGGGGGGGCCC
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Program for Rat Gene Discovery and Mapping
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/db_xref="taxon:9606"
/clone="UI-E-EJ1-ajk-j-22-0-UI"
/clone_lib="UI-E-EJ1"
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/dev_Stage="fetal and adult"
//dev_Stage="fetal and adult"
//lab_host="DH10B (Life Technologies) (TI phage resistant)"
//note="Organ: eye; Vector: pTT3-Pac (Pharmacia) with a modified polylinker; Site_1: ECOR I; Site_2: Not I;
UI-E-EJ1 is a subtracted cDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an ECOR I adaptor, digested with Not I, and cloned directionally into pT773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are: fetal eyes, AGAPICAAGA; lens, CGATTAGCGA; eye anterior segment, AATGCCGAT; optic nerve, CCATTAAGTG; retina, CGGCG; Retina Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This library was created for the program, Gene Discovery in the Visual Eye Institute (NEI).
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UI-E-EJO-ahn-h-16-0-UI.sl UI-E-EJO Homo sapiens CDNA clone
UI-E-EJO-ahn-h-16-0-UI 3', mRNA sequence.
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Pred. No. 1.2e-103; .
0; Mismatches 9; Indels
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TAG_TISSUE-RPE and Choroid
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185 c 1
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98.2%;
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121 GFGAAACGFGCAFCCCGAGGGCTFCTAGGAFGAAGFAGTCCACFGGAAGGCACCAGCTCF 180
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//ab_host="DH10B (Life Technologies) (TI phage resistant)"

//ab_host="DH10B (Life Technologies) (TI phage resistant)"

//note="Organ: eye; Vector: pT73 Pac (Pharmacia) with a
modified polylinker; Site_1: ECOR I; Site_2: Not I;
UI-E-EJO is a subtracted cDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an ECOR I adaptor; digested
with Not I, and cloned directionally into pT77-pc
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)1B tail. The
sequence tags for this library are: fetal eyes, AGAATCAAGA
; lens, CGATTAAGTG; retina, CGGG; Retina Foveal and
Macular, GTCC; RPE and Chorold, ACCTA. This library was
created for the program, Gene Discovery in the Visual
System, supported by National Eye Institute (NEI).
TAG_LIB-UI-E-EJO
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                                                                                                                                                                                                                                                                                                                                                                                                     Email: msoares@blue.weeg.ulowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing.Dy: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
                                                                                      Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo.
1 (bases 1 to 631)
                                                                                                                                                        Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clome="UI-E-EJO-ahn-h-16-0-UI"
/clome_lib="UI-E-EJO"
/tissue_type="fetal eyes, lens, eye anterior segment,
optic nerve, retina, Retina Foveal and Macular, RPE and
                                                                                                                                                                                                                                                                                                                 University of Iowa 451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250 Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180 CCCCTCCTCCAGGGGTATCCCCTCTTTCTAGGGACCTACCCAAGCTAGGCCTTTCTTCCA 239
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Program for Rat Gene Discovery and Mapping
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/db_xref="taxon:9606"
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184 c 168 q
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Seg primer: M13 Forward
POLYA-Yes.
  BM675116.1 GI:18985014
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                                                                      Homo sapiens
                                                                                                                                                                                                       discovery
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VERSION
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CMV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BI759786 1797 bp mRNA linear EST 25-SEP-2001 603045668F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5185961 5',
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 797)
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        24.1
        GAGACACCTTGGGGGGGCTTTGCTCGCGGAACACGCGCAGAGCGTGGGGAGGAGGGCCC
        300

        360
        GAGACACCTTGGGCGGGGCCTTTGCTCGCCGGAAGCACGCAGAGCGTGGGGAGGAGGAGGGGC-CC
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181 TCCTTTTATCTCTCCAGAGCTGGACAGTGCACCAGGGGCCGGTACTGGTTCCCCAGCTAG 240
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/clone="IMAGE:5185961"
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BI759786
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Unpublished (1997)
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                                                    10;
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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                                                                                                     TITCTAGGGACCTACCCAAGCTAGGCCTTTCTTCCAGTG----AAACGTGCATCCCGAGG
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 a NIH_MGC Library."
                                 Score 482; DB 13; I
Pred. No. 1e-100;
0; Mismatches 35;
Note: this is 280 c 234 q
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                                   48.28;
92.58;
                                          al Similarity 92.5
618; Conservative
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                                          Best Local
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AUTHORS
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/Organism="Homo sapiens"
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/dav_stage="Research"
/da
Contact: Robert Strausberg, Ph.D.
Email: cgapbs.remail.nih.gov
Tissue Procurement: Dr. Steven Brown
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@ulowa.edu
BoltA-Yes.
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Best Local Similarity 97.5%;
Matches 433; Conservative
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RESULT 11 AW139412

ACCESSION

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KEYWORDS SOURCE

REFERENCE AUTHORS

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UI-E-EJG-aii-i-18-0-UI.SI UI-E-EJG Homo sapiens CDNA clone UI-E-EJG-aii-i-18-0-UI 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 556)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Normalization and subtraction: two approaches to facilitate gene
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Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
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TAG_TISSUE=colon
TAG_SEQ=AAACG"
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ilarity 97.3%;
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/dlone='Inbacs:2717670"
/clone='Inbacs:2717670"
/clone='Inbacs:2717670"
/clone='Inbacs:2717670"
/lab_host="DH10B (Life Technologies)"
/lab_host="DH10B (L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-remail.ih.gov
The sequence contained an oligo-dr track that was present in the oligonuclectide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A Ltail. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
                                                                                                                                                                   AW139412 554 bp mRNA linear EST 30-OCT-1999 UI-H-BII-adq-e-04-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717670 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 554)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      www-bio.llnl.gov/bbrp/image/image.html
Seg primer: M13 Forward
POLYA-Yes.
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AW139412.1 GI:6144130
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FEATURES

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530 bp mRNA linear EST 16-OCT-2000
TK69C04.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3480582 3',
DF061934
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center DNA Sequencing DY: Washington University Genome Sequencing Center Clone distribution: NCI-GGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to:
                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                   1 (bases 1 to 530)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/tissue_type="pooled germ cell tumors"
/lab_host="DH108"
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41.0%; Score 409.6; DB 12;
Best Local Similarity 97.9%; Pred. No. 4.2e-84;
Matches 415; Conservative 0; Mismatches 9;
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Seq primer: -400P from Glbco
High quality sequence stop: 459.
Location/Qualifiers
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/clone="IMAGE:3480582"
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Unpublished (1997)
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// lab_host="Parlob (Life Technologies) (TI phage resistant)"

// lab_host="DH10B (Life Technologies) (TI phage resistant)"

// lab_host="DH10B (Life Technologies) (Tharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-E-EJO is a subtracted cDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dry primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I; and cloned directionally into pT773-pac vector. The oligonolectide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are: fetal eyes, AGAATCAAGA; lens, CGATTAGCGA; eye anterior segment, AATGCCGAT; optic nerve, CCATTAAGTG; retina, CCGC; Retina Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This library was created for the program, Gene Discovery in the Visual System; supported by National Eye Institute (NEI).
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42.3%; Score 422.6; DB ]
Best Local Similarity 97.9%; Pred. No. 4.3e-87,
Matches 428; Conservative 0; Mismatches 9
                                             Location/Qualifiers
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Seq primer: M13 Forward
POLYA=Yes.
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/lab_host="ToplOF"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        44b bp mRNA linear EST 06-MAR-2002
MRNA sequence.
BM849644
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 446)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                         obtained cDNA vectors were used for transformation of
                        CCTCTGCCTGTGTTTGTGCCAAACAGCACCCGCGCTGCCGCGCTCGGGTTCCGGCGGCGGCGGA
                                                                                                                                              GTCACACATGATGTCACAGACAATGACACAAGCCGGTGTCTCATTCCGACACAGGGTCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Roeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4409
Fax: +82-42-860-4409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: yongsung@mail.kribb.re.kr
Plate: 36 row: A column: 07
High quality sequence stop: 446.
Location/Qualiflers
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Length 446;

Score 406; DB 14; Pred. No. 2.7e-83;

40.6%;

Query Match Best Local Similarity

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

I (bases 1 to 543)

I (bases 1 to 543)

S Hillaer,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,

Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B.,

, Cochalenbergy, K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylle
,T., Waterston,R. and Wilson,R.

MashU-Merck EST Project 1997

L Upublished (1997)

Contact: Wilson RK

WashIngton University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1810

Fax: 314 286 1810
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@inage.llnl.gov) for further information.
Seq primer: -41ml3 fwd. ET from Amersham
High quality sequence stop: 469.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                           514
                                                    275 CACGCAGAGCGTGGGGAGGAGGCCCCCTCTGCCTGTGTTTGTGCCAACAGCACCGCGC 334
                                                                                                                                                       335 TGCCGCGTCGGGTTCCGGCGGCGGGGGTCACATGATGTCACAGACAATGACAAAGCC 394
                                                                                                                                                                                    395 GGTGTCTCATTCCGACACACAGCGTCCGAGCTGCACAATGTCACACCCGGGTGCCAAACACT 454
                                                                                                                                                                                                                                                                                                       267
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  Gaps
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Indels
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AA404273.1 GI:2058997
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(Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT773 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo. " 148 c 143 g 134 t 1 others
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                                                                                                                                                           CCCTCTGCCTGTGTTTGTGCCCAACAGCACCGGGTGCCGCGTCGGGTTCCGGCGGCCGG 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGTCACACATGATGTCACAGACAATGACACAAGCCGGTGTCTCATTCCGACACAGCGTCC 419
                                                                                                                        Gaps
                                                                                                                                              1 GTCCTTGGGTAGCATGTACATTTCCATCCCTTCCTTTTATATATGGGGGTAATAGGATAC 60
Double-stranded cDNA was ligated to Eco RI adaptors
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                                                                                                                       2;
                                                                                                Length 543;
                                                                                                                       Indels
                                                                                               Score 393.8; DB 9;
Pred. No. 1.9e-80;
0; Mismatches 13;
                                                                                             Query Match 39.4%;
Best Local Similarity 96.6%;
Matches 423; Conservative
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                                                           117
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Search completed: March 30, 2003, 13:48:06 Job time : 1296.28 secs

March 30, 2003, 08:00:38 ; Search time 2122.53 Seconds (without alignments) 13725.086 Million cell updates/sec US-09-691-220-3_COPY_5000_6000 1001 1 tgatctcccctcccccacc.....tgggtcaccctctggctg 1001 4109280 GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd. Total number of hits satisfying chosen parameters: 2054640 seqs, 14551402878 residues OM nucleic - nucleic search, using sw model Post-processing: Minimum Match 0%
Maximum.Match 100%
Listing first 45 summaries IDENTITY_NUC Gaport 1.0 em_htg_other:* em_htgo_hum:* em_htgo_mus:* Minimum DB seq length: 0 Maximum DB seq length: 2000000000 em_htg_hum:* em_htg_pln:* em_htg_rod:* em_htg_mam: em_htq_mus: gb_pr:* gb_ro:* gb_sts:* em_fun:* em_sts:* em_un:* gb_ba:* gb_htg:* gb_in:* gb_sy:* gb_un:* gb_vi:* gb_om:* gb_ov:* gb_pat:* gb_ph:* em_in:* em_om:* em_ro:* em_vi:* em_mu: em_ov: em_pl: gb_p1:4 em_pat GenEmbl:* Title: Perfect score: Sequence: Scoring table: Database : Searched: Run on:

is the number of results predicted by chance to have a Pred. No.

em_htgo_other:*

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

S . Description	8 Homo sap	6 Homo sap	Homo:	2 HOMO Sap 3 Homo sap	2 Homo sap	ance	Human 6 Ratt	7 Mus mu	KAKA=rec 5 Homo s	4 Rattus	Sequence	w.	5 Homo s	3 Rattus	4 Homo s	7 Rattus 6 Rattus	8 Homo s	6 Rattus 2 Rattus	4 Rattus	O Rattus 8 Mus mu	7 Rattus	നഗ	7 Rattus	s Kattus 9 Human	2 Rattus	9 Mus musc	6 Rattus	4 Rattus n	* Rat	3 Rattus n	S		intron 2.	alpha.		aniata; Vertebrata; Buteleostomi; tarrhini; Hominidae; Homo.		
SUMMARIES	HSA297538	AC015851	AC018629	AC131063	AC126392 AX344790	AX344791		AL591067	AF429315	AC119084 AC109005	166494	AC020738	AC084075	AC099003 AC096234	AC011674	AC111607 AC130936	AC022648	AC126076 AC121212	AC128784	AC126730 AL772338	AC123357	AC027353 AF429315	AC111697	AL731559	AC128072	AC116109	AC129706	AC1106174	AC108286	AC095743	ALIGNMENT		gene,	223 acid receptor		ca; Cr	ter,A.	
Length DB	16913	38399 58766	6368	88574	90309 13508	13508 6		31248	25020	626	7218	4520	61633	1473 8928	6822	1204	85268	17082 65988	91277		68280	01509 25020	38467	96320	74845	68330	9771	83334	54677	365			ns partial	GI:12054; retinoic		Metazoa; utheria;	to 16913 , and Rei	i to 16913)
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	1 10	10	4 10	201	10 584	c 9 507	146	140	14 59	15	17	51	50	22 48	8 1	25 46	26 46	4 4	29 46	4 4 6 0	46		45	45	38 45	4.5	41 45	. 7	44	45 44				VERSION A			REFERENCE I AUTHORS C	
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ACO90426 138999 bp DNA linear PRI 29-MAY-2002 Homo sapiens chromosome 17 clone 205m17 map 17q21.1, complete sequence.
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                                                                                       15825 CCTAGGGAGGCATCCTCATCCATCCTTGGCCCTGGACAAGAGAACTTGAACGTTGGTAGG
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                                                 15405 GGCATCAACTGTCCCATTGCTGCAGGCTGGTCTTGGGGCAGGGGATGGGGGGGCA
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                                 GGCATCAACTGTCCCATTGCTGCAGGCTGGTCTTGGGGGCAGGGAAGGGGATGGGGGGGCCCA
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             Direct Submission
Submitted (07-AUG-2000) Cross N.C.P., Department of Haematology,
Imperial College School of Medicine, Hammersmith Hospital, London,
W12 ONN, UNITED KINGDOM
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REFERENCE 2 (bases 1 to 138999) AUTHORS GU, B., Xlong, H., Zhou, Y., Chen, B., Lu, L., Zhong, M., Yin, H., Huang, W., Ren, S., Chen, S.F., Chen, Z. and Fu, G. TYTLE Direct Submission JOURNAL Submitted (20-FEB-2001) Chinese National Human Genome Center at Shanghai, Shanghai, Shanghai, Shanghai, Shanghai, Shanghai 201203, P.R. Chinese COMMENT Center: Chinese National Human Genome Center at Shanghai	Center code:CBGC Website: http://www.chgc.sh.cn Contact: fugang@chgc.sh.cn. FEATURES Location/Qualifiers 1. 138999 /organism="Homo sapiens" /db_xref="faxon:9606" /map="17011.1"	repeat_region 10331198 repeat_region 12171514 /rpt_family="SINE/Alu" /rpt_family="SINE/Alu" /rpt_unit=AluSp repeat_region complement(15341754)	repeat_region 2291 .2366 /rpt_tanily="SINE/MIR" /rpt_family="SINE/MIR" /rpt_tanily="SINE/MIR" repeat_region complement(2607 .2665)	repeat_region 351. 3905 /rpt_family="LINE/L1" /rpt_tamily="LINE/L1" /rpt_unit=LIME2 repeat_region 3977. 4029 /rpt_tamily="LINE/L1" /rpt_tamily="LINE/L1" /rpt_unit=LIME2 repeat_region 4030. 4219	repeat_region 42144509 /rpt_anily="SINE/Alu" /rpt_anily="SINE/Alu" /rpt_anily="SINE/Alu" /rpt_family="SINE/Alu" /rpt_family="SINE/Alu"	repeat_region /rpt_family="LTR/MalR" /rpt_unit=MSTD repeat_region 5019. /rpt_family="LINE/LI" /rpt_unit=LINE/LI" /rpt_unit=LINE2 repeat_region 5236. 5443 /rpt_family="SINE/MIR"	repeat_region 5467.5699 /rpt_danily="SINE/MIR" /rpt_unit=MIR /rpt_unit=MIR /rpt_tamily="SINE/MIR" /rpt_tamily="SINE/MIR" /rpt_unit=MIR /rpt_family="Low_complexity" /rpt_tamily="Low_complexity" /rpt_tamily="SINE/MIR" /rpt_tamily="SINE/MIR" /rpt_tamily="SINE/MIR"

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Spirren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Balren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Heaford, A., Horton, L., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrin, J., Merterson, K., Pollara, V., Riley, R., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X.,
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Homo sapiens chromosome 17 clone RPS-1112G21 map 17, WORKING DRAFT
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Submitted (17-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 8, 2001 this sequence version replaced gi:13123358.
All repeats were identified using RepeatMasKer: Smit, A.F.A. & Green, P. (1996-1997)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                     http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 17, clone RP5-1112G21 Unpublished
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         Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                             Sequencing vector: M13; M7815; 41% of reads Sequencing vector: Plasmid; L08752; 4% of reads Sequencing vector: Plasmid; L08752; 4% of reads Sequencing vector: Plasmid; L08752; 4% of reads Chemistry: Dye-primer-amersham; 12% of reads Assembly program: Phrap; verston 0.960731 Consensus quality: 155148 bases at least Q40 Consensus quality: 155118 bases at least Q30 Consensus quality: 155118 bases at least Q30 Insert size: 63000; agarose-fp
                                      Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
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2774: gap of 100 bp
3397: contig of 623 bp in length
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                                                                                                                                                                                                                 Length 158766;
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100.0%; Pred. No. 3.3e-267;
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Center: Whitehead Institute/ MIT Center
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Homo sapiens chromosome 17 clone RP11-5809 map 17, *** SEQUENCING
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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (14-DEC-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 3 (bases 1 to 166368)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 166368)
                                                                    78508 CCAGCCCTGTTCTGCCTACAGTGATGGCCATGGAGCCAGACACTGGGGGAGGATTTGGCCA 78567
          CCAGCCCTGTTCTGCCTACAGTGATGGGCCATGGAGCCAGACACTGGGGAGGATTTGGCCA
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Homo sapiens chromosome 17, clone RP11-5809
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2089 CITCCITCCTCTGTGCCCCAAITTTAGGCCCATGTGATTTGGGGCTATGTGACTCATGTC 2148
for Genome Research
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                                                                                                                                                                              NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TGATCTCCCCTCCCCCCACCAGTCTGGATTGTCTATTGTTACTGCTTTTACGTCTTGGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 166368;
                                                   Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------- Project Information
Center project name: L924
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39988 a 40877 c 42066 g 43337 t 100 others
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83946 166368: contig of 82423 bp in length.
Location/Qualifiers
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Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens chromosome 17 clone CTD-2267D19 map 17, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthería; Primates; Catarrhini; Hominidae; Homo.
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Barna,N., Bastlen,V., Bloom,T., Boguslavkiy,L., Boukhgalter,B.,
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                                                                                                                                                                2449 CCAGCCCTGTTCTGCCTACAGTGATGGGCATGAGGAGCCAGACACTGGGGAGGATTTGGCCA 2508
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                                  2269 CCTAGGGAGGCATCCTCATCCATCCTTGGCCCTGGACAAGAGAACTTGAACGTTGGTAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                        2389 TATCTTGCACCCAACACTTAGCTGCCCAGGCTTTGGACATGGATAGCCCCTACCCAAC
                                                                                                                              GGAGTTTGGGGTAGGCTAGGTAGGATTGTGGAATATGGGAGGAGGCAGGGATCTGTCTA
                                                                                                                                                                                                                                                                CCTAGGGAGGCATCCTCCATCCTTGGCCCTGGACAAGAACTTGAACGTTGGTAGG
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GCCTCAGGACGATGCTGCGTGGCCCCTTGGGAATCTGGGATTGTCCTGGTCATAGTTCT
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HTG; HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN.
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Unpublished
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Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Fare, S., Ferreira, P., FitzGerald, M., Gadge, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Lilev, I., Johnson, R., Jones, C., Kamat, A., Kals, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLens, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Meldrin, J., Meneus, L., Mihowa, T., Medga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Oilver, J., Peterson, K., Phunkhang, P., Pierre, W., Raymond, C., Retta, R., Seaman, S., Severy, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Viel, R., V., Allson, B., Tayers, M., Vassiliev, H., Zinmer, A. and Zody, M., Waman, D., Young, G., Zainoun, J., Zembek, L., Zinmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (14-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 14, 2002 this sequence version replaced gi:22123315.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
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Center: Whitehead Institute/ MIT Center for Genome Research
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Pred. No. 3.3e-267;
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/db_xref="taxon:9606"
/chromosome="17"
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/clone_lib="CITD1 Human
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                   GCCATCAACTGTCCCATTGCTGCAGGCTGGTCTTGGGGGAAGGGGGATGGGGGGCCCA
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                                     GTGAAGAGCAGACGCCGTGGGGAGGTCAGGAGAATCTGCTGGGCTGGGGATGGTGTG
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Homo sapiens chromosome 17, clone RP11-1029L16
Unpublished
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HTG; HTGS_PHASE1; HTGS_ROLLTOP.
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Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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2073 2172: gap of 100 bp
2173 19348: contig of 17176 bp in length
21349 19448: gap of 100 bp
34798: contig of 15350 bp in length
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Nightonian Cook, P. (Deases 1 to 190309)

Be Birren, B., Nusbaum, C., Lander, E., All, A., Allen, N., Anderson, S., Barren, B., Nusbaum, C., Lander, E., Bogualavkiy, L., Boukhgalter, B., Canaraca, J., Chang, J., Chazaro, B.; Choepel, Y., Collymore, A., Cook, A., Coke, P., DeArellano, K., Dewar, K., Dlaz, J.S., Dodge, S., Faro, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Harcon, E., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Liley, I., Johnson, R., Jones, C., Kanat, A., Karatas, A., Kalls, C., Maddens, T., Matchews, C., Norman, J., MacLean, C., Madden, P., MacLean, C., Madden, P., Matchews, C., Norman, C., Madlan, J., Menels, L., Minova, T., Matchews, C., Norman, J., Noy, D., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Vell, R., Vo, A., Wilson, B., Wux, Travers, M., Vassiliev, H., Labmiss, D., Voll, R., Vo, A., Wilson, B., Wux, T., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Lungh, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Lembas, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Viel, R., Washam, C., Diaz, J.S., Dodge, S., Gangas, I. to 19309)

Liect Submission

Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C., Mant, A., Karatas, A., Kells, C., Lander, F., Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C., Murphy, T., Washam, C., Macdonald, P., Major, J., Matthews, C., Murphy, T., Waylor, J., Maynon, C., Rette, R., Senan, S., Severy, P., Karatas, A., Kells, C., Landers, T., Levine, R., Massilie, W., Phunkhang, P., Pierre, M., Raymond, C., Rette, R., Senan, S., Severy, P., Rungh, P., Pierre, M., Raymond, C., Rette, R., Senan, S., Severy, P., Rungh, P., Pierre, B., Stange-Thoman, W., Yell, R., Yo, A., Wilson, B., Wu, X., Waynan, C., Volly, Wolly, C., Spencer, B., Stanger, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC126392 190309 bp DNA linear HTG 06-AUG-2002 Homo saplens chromosome 17 clone RP11-1029F16 map 17, WORKING DRAFT SEQUENCE, 11 ordered pieces.
                                                                                                                                                                                                                                                                                                      DD 159940 CCAGCCCTGTTCTGCCTACAGTGATGGGCATGGAGCCAGACACTGGGGAGGATTGGCCA 159881
                                                                                                                                                                  160000 TATCTTGCACCCAACACCTTAGCTGCCCAGGCTTTGGACATGGATAGCCCCTACCCAAC 159941
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                  160060 GGCCTCAGGACGATGCTGCGTGGCCCCTTGGGAATCTGGGATTGTCCTGGTCATAGTTCT
                                                                                                                                   841 TATCTTGCACCCAACACCCTTAGCTGCCCAGGCTTTGGACATGGATAGCCCCTACCCAAC
                                                                                                                                                                                                                                                                       901 CCAGCCCTGTTCTGCCTACAGTGATGGGCATGGAGCCAGACACTGGGGAGGATTTGGCCA
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Birren, B., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 17, clone RP11-1029F16
Unpublished
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                                      Center for Genome
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Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. Gaps between the contigs are represented as runs of N. The order of the pleces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
             Direct Submission
Submitted (06-AUG-2002) Whitehead Institute/MIT Center for
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Aug 6, 2002 this sequence version replaced g1:21699357
                                                                                                                                                                                                                                                                                                                                                                                                                          Insert size: 179000; agarose-fp
Insert size: 189309; sum-of-contigs
Quality coverage: 15: 5 in Q20 bases; sqarose-fp
Quality coverage: 15: 6 in Q20 bases; sum-of-contigs
                                                                                    All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                       Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108284 130510: contig of 22227 bp in length 130511 130610: gap of 100 bp 130611 166740: contig of 36130 bp in length 166741 166840: gap of 100 bp 166841 190309: contig of 23469 bp in length 1. . 190309: contig of 23469 bp in length.
                                                                                                                                                                                                                                                                                            Sequencing vector: Plasmid; n/a; 100% of reads Sequencing vector: Plasmid; n/a; 100% of reads Assembly; Dye-terminator Big Dye; 100% of read Assembly program: Phrap; version 0.960731 Consensus quality: 18751 bases at least 030 Consensus quality: 188537 bases at least 030 consensus quality: 188537 bases at least 020
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33794 35405; contig of 1612 bp in length
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Center clone name: 1029_F_16
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Zembek, L., Zimmer, A. and Zody, M.
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41975 GCCATCAACTGTCCCATTGCTGCAGGCTGGTCTTGGGGCAAGGGGAAGGGGATGGGGGCCCA 42034
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/note="assembly_fragment"
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/note="assembly_fragment"
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66115. .108183 /
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108284. .130510 /
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           42395 CCTAGGGAGGCATCCTCATCCATCCTTGGCCCTGGACAAGAGAACTTGAACGTTGGTAGG 42454
                                                      TGCAGGCTGGTCTTGGGGCAGGGAAGGGGATGGGGGGCCATAGCAGTGCTGGTCAGCCAG 380°
                                                                                       TATCTTGCACCCAACACCCTTAGCTGCCCAGGCTTTGGACATGGATAGCCCCTACCCAAC 900
                                                                                                                                   CCAGCCCTGTTCTGCCTACAGTGATGGGCATGGAGCCAGACACTGGGGAGGATTTGGCCA 960
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 CCTAGGGAGGCATCCTCCATCCTTGGCCCTGGACAAGAACTTGAACGTTGGTAGG
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Diagnosis of diseases associated with development genes
Patent: WO 0200927-A 215 03-JAN-2002;
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Location/Qualifiers
Location/Qualifiers
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/organism="synthetic construct"
/db_xref="taxon:32530"
/note="chemically treated genomic
/note="chemically treated genomic
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Pred. No. 2.5e-151;
0; Mismatches 248;
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Sequence 215 from Patent W00200927.
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Local Similarity 74.7%;
Les 733; Conservative 0
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                                                                                                                                     861 TAGCTGCCCAGGCTTTGGACATGGATAGCCCCTACCCAACCCAGCCCTGTTCTGCCTACA
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                                                           TTGGCCTAGTTCCCTGTCATCAGCCGCCTAGCAGCCCCCACTGTGTCTGCAGGTAAGGGG
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                                                                           ATTTTAGGGCCATGTGATTTGGGGCTATGTGACTCATGTCTGTAAGGTGCTTGGGCCAGG
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Diagnosis of diseases associated with development genes
Patent: WO 0200927-A 216 03-JAN-2002;
Epigenomics AG (DE)
Location/Qualifiers
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/db_xref="taxon:32630"
/note="chemically treated genom
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1 TGATCTCCCCTCCCCCACCAGTCTGGATTGTCTATTGTTACTGCTTTTACGTCTTGGAA 60

L17737.1 GI:957208 STS; STS sequence; primer; sequence tagged site.

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1810 TAATCTCCCCCCCCCCCCATTAATTATTATTACTATTTATAGGTCTTAAAAA 1751
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                                                                  121 AGGCCCCCCAACCCCCCCCCCCCCCAGCAGCTGTTCTCAGGCCTCTCAGCCTGTCTGATTTG 180
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                            AAAGTTAGCACAACAAAGGGCTGCTTTGTGGCTCACCCCCTCTGCCTCCTGGCCTCACCC 120
                                                                                                                                               GTGAAGAGCAGACGCCGGTGGGGAGGTCAGGAGAATCTGCTGGGGCTGGGGATGGTGTG 300
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Pred. No. 1.1e-95;
0; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : Acrylamide 7%, Formamide 32%, Urea
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/standard_name="STS UT5218"
171. 189
complement(303. 321)
105 c 163 g 128 t

    .516
    /organism="Homo sapiens"
/db_xref="taxon:9606"

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Annealing: 62C 10sec
Extension: 72C 20sec
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89.1%;
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Best Local Similarity 89.1
Matches 457; Conservative
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                                                            Homo sapiens.
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PCR Profile:
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Gel: Acrylam
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STS 26-SEP-1995

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HUMUT5218 516 bp DNA Human STS UT5218, sequence tagged site. L17737

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*** SEQUENCING IN PROGRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                565 TAGGGCCATGTG---ATTTGGGGCTATGTGACTCA--TGTCTGTAAGGTGCTTGGGCCAG 619
                                                     DNA
                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus clone CH230-15011,
***, 72 unordered pieces.
AC111746
                                                                                                                                                                                       481 AGNTTINGGCAACCTINAAATTGCANCCANINT 513
                                                                                                                                               620 GAGCTGTGGGCACCTTTAAATGCCAGCCAGTCT 652
                                                                                                                                                                                                                                                                                                                                                                           162393 bp
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* NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a "working draft' sequence. It currently

* Consists of 7 contigs. The true order of the places

* is not known and their order in this sequence record is
Direct Submission
Submitted (13-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, Tx 77030, USA on Jul 12, 2002 this sequence version replaced gi:18701588.

Center: Baylor College of Medicine
                                                                                                                                                                                                                                                                                                                                                    arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                          Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
                                                                                                                                                                                                                  Assembly program: Phrap; version 0.990329
Consensus quality: 96609 bases at least Q40
Consensus quality: 101360 bases at least Q30
Consensus quality: 105362 bases at least Q20
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                                                                                                          Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
------- Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                       1342: gap of unknown l
2427: contig of 1085 bg
2527: app of unknown l
3635: contig of 1108 bg
3735: gap of unknown l
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112215 ACAAAGGACTCCTTTGTCACTCCTTTGCCTCCTGGCCTCACGGCCCCCCCAA 112274
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                                                                                  133 CCGCCCCCCAGCAGCTGTTCTCAGG----CCTCTCAGCCTGTCTGATTTGCTTGTTG 188
                                                                                                                                          189 GCCTGGGGAGAATGAGGT--GGGAGAAACCAGGCCAGGGCAGTT-GGTGTTGGAGTGAA 245
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KEYWORDS
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Best Local Si
Matches 309;
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231248 bp DNA linear HTG 09-AUG-2002 Mus musculus chromosome 11 clone RP23-333D2, *** SEQUENCING IN AL591067
                                                                                                                                                                          Db 112395 CAGCAGATTGCAGCTGGTCAGTCCTCTG-----GACCCTTGGGGGGTTGTAGGCAC 112445
                                                                                                                                                                                                                                                                                                                                                                                                                                             Db 112492 ATGCTGGACCGCCCGGC-----TGATGTCCAGGCCCAAGTAGGAGCCAGGAA 112539
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 231248)
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Direct Submission

Submitted (30-JUL-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Aug 11, 2002 this sequence version replaced g1:19848047.

Center: Wellcome Trust Sanger Institute
112335 GCCTCCTGAGAAGGAAGTGAGAAAAACCAGGGCAGAGCAGAGCAGTTCTGTGTAGAGGATGAG 112394
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Sequencing vector: plasmid; 108752; 100% of reads
Chemistry: Dye-terminator; 1% of reads
Consensus quality: 231046 bases at least Q40
Consensus quality: 231133 bases at least Q30
Consensus quality: 231138 bases at least Q30
Insert size: 231146; sum-of-contigs
Insert size: 231544; 2.5% error; agarose-fp
Quality coverage: 11.33x in Q20 bases; sum-of-contigs Quality
coverage: 11.16x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                             112446 CGATGAGTCCTTTCCCTCTGGTTAGAGAGGGGACA--------TGGTTACAGCA 112491
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                                                                                                    246 GAGCAGACGCGGTGGGGAGGTCAGGAGAATCTGCTGGGCTGGGGATGGTGGGGCAT 305
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HTG: HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.
house mouse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112540 GICCTGCCAAGGCCATTGGCAGAGTTCCCGGT 112571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center code: SC
Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center project name: bM333D2
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Conservative

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Best Local Similarity 98.6%;
Matches 71; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S57794 914 bp DNA linear PRI 28-JUN-1993 RARA-retinoic acid receptor alpha [3' region of 2nd intron, 5' end of 3rd exon, region flanking translocation breakpoints} [human, Genomic, 914 nt].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DD 142888 CCCCCCTAAGTCTGGATTGTCTATTGTTACTGCTTTTACGCTCTTGGAAAAGTTAGCACA 142947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db 142948 ACAAAGGGCTCCTTGTCACTCCTTGCCTCCTGGCCTCACCCAGGCCCCCCAAC 143007
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Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 914)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DD 143068 GGGCCTCCCGRQBAGGAAGTGAGGAABACTGGGGCAGGGCAGTTGTGTGTGTGTAGGCATGA 143127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db 143128 GCAGCAGATTGCAGCAGGTCAGTCCTTTGGACCCCTGGGGGTTGTAGG------ 143175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       143008 CCGCCCCCCAACCCCCAGCAGTGTTGTCAGGCCTCCGCCTGTTTGATTTGCCTGTCG 143067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db 143176 ------CATGGAAAAGTCCTTTTCCATGGGTTAAAGAAGGGAACATGGGTTACAGC 143225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73 ACAAAGGGCTGCTTTGTGGCTCACCCCCTCTGCCTCGGCCTCACCCAGGCCCCCCAAC 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            187 IGGCCTGGGGAGAATGAGGTG-GGAGAAAACCAGGCCAGGGCAGTTG-GTTGGAGTGA 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      133 CCCGCC-----CCCCCAGCAGCTGTTCTCAGGCCTCTCAGCCTGTCTGATTTGCTTGTC 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         305 TCAACTGTCCCATTGCTGCAGGCTGGTCTTGGGGCAGGGGAAGGGGATGGGGGCCATAGC 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   245 AGAGCAGACGCCGTGGGGAGGTCAGGAGAATCTGCTGGGGCTGGGGATGGTGTGGGCA 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                365 AGTGCTGGTCAGCCAGGCTGGGCAAGTGGTGCCCAGGCACTACTAAGAGCCAGGAA 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 CCCCCACCAGTCTGTGTTTTTACTGCTTTTACGTCTTGGAAAAGTTAGCACA 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                    42; Gaps
arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 231248
                                                                1 134201: contig of 134201 bp in length 134202 134301: gap of 100 bp 100 bp Location/Qualifiers 1. 231248
                                                                                                                                                                                                                                                                                                                                                       100 others
                                                                                                                                                                                                                                                                                                                                                                                                              Score 140.4; DB 2; Length
Pred. No. 5e-28;
0; Mismatches 111; Indels
                                                                                                                                                                                                                                                                          1. 134201
/note="assembly_fragment:06314"
134302. 231248
/note="assembly_fragment:07956"
1 56205 c 57206 g 62207 t
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                                                                                                                                                                                       /organism="Mus musculus"
                                                                                                                                                                                                      /db_xref="taxon:10090"
/chromosome="11"
                                                                                                                                                                                                                                                           /clone_lib="RPCI-23"
                                                                                                                                                                                                                                          /clone="RP23-333D2"
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 14.0%;
Best Local Similarity 66.2%;
Matches 299; Conservative (
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S57794.1 GI:299073
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VERSION
KEYWORDS
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Holmes, S.E., O'Hearn, E., Rosenblatt, A., Callahan, C., Hwang, H.S., Ingersoll-Ashworth, R.G., Fleisher, A., Stevanin, G., Brice, A., Arepeat expansion in the gene encoding junctophilin-3 is associated with Huntington disease-like 2 (4), 377-378 (2001)
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Holmes,S.E., Ingersoll-Ashworth,R.G., Ross,C.A. and Margolis,R.L.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        exon 3"
                                                                                                                                                                                                                           GenBank staff at the National Library of Medicine created this entry [NCBI glbbsq 129120] from the original journal article. Location/Qualifiers
                                                                                                     the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
Dong, S., Geng, J.P., Tong, J.H., Wu, Y., Cai, J.R., Sun, G.L., Chen, S.R., Wang, Z.Y., Larsen, C.J., Berger, R. et, al. Breakpoint clusters of the PML gene in acute promyelocytic leukemia: primary structure of the reciprocal products of the PML-RARA gene in a patient with t(15,17) Genes Chromosomes Cancer 6 (3), 133-139 (1993) 7682097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (05-OCT-2001) Psychiatry, Johns Hopkins Medical
Institutions, 600 N. Wolfe St., Baltimore, MD 21287, USA
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="16q24.3; between D16S520 and WI-12410"
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Homo sapiens junctophilin 3 (JPH3) gene, partial cds.
AF429315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="retinoic acid receptor alpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note-"retinoic acid receptor alpha"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 60; DB 9;
Pred. No. 1.4e-05;
0; Mismatches 0
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/codon_start=1
/protein_id="AAD1388.1"
/db_xref="G1:4261588"
/translation="PLRPRAAVLKR"
> 242 c 286 g 215 t
                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                    880. .914
/partial
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132731 c 30696 g 28283 t 4254 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17629 KRSYYYWGGGRRAKKKYYCAGRRRRMSYWKCCAKWWMSYCCWSYCMTYYSKSCTYKSST 17570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | :| ::::| :: |:::| :: 17509 AGWGAGWRSSKGKRSTGMKRACSKKTGSYGSTGRSMKKKKGYSKVSRGMKGKKKTCYCMW 17450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SYKSYKKGRGKMKGWGGMKRGSKINSSMKKMKRSSWSKCISTKSIKSGRRKSKGWGRSTK 17270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          256 CGGTGGGGAGGTCAGGAGAATCTGCTGGGCTGGGGATGGTGTGGGGCATCAACTGTCCC 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAGAATGAGGTGGGAGAAAACCAGGCCAGGGCAGTTGGTGTTGGAGTGAAGAGAGCAGACGG 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTGCTGCAGGCTGGTCTTGGGGCAGGGGAATGGGGGGGCCATAGCAGTGCTGGTCA
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/note="isolated from a patient with Huntington's Disease-Like 2 (HDL2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 5.9%; Score 59.2; DB 9; Length 125020; Best Local Similarity 12.7%; Pred. No. 1.9e-05; Matches 102; Conservative 339; Mismatches 356; Indels 8;
                                                                                                                                                                                                                                                                                                                        membrane and endoplasmic reticulum"
                                                                                                                                                                                    .>36887)
                                                                                           /rpt_unit=ctg
complement(<36507. .>36887)
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                                                                                                                                                                                                                                                                                                                                                /codon_start=1
/product="junctophilin 3"
                       Disease-Like 2 (HDL2)"
complement(35581. .35746)
                                                                                                                                                                                                                            /product="junctophilin 3"
                                                                                                                                                                             complement(<36507.
/gene="JPH3"
                                                                      /rpt_type=tandem
                                                                                                                                     /gene="JPH3"
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                                              repeat_region
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Submitted (25-APR-2002) Human Genome Sequencing Center, Department
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                      732 ATCCTCAT----CCATCCTTGGCCCTGGACAAGAGAACTTGAACGTTGGTAGGGGCCTCA 787
                                                                                                                             788 GGACGATGCTGCGTGGCCCCTTGGGAATCTGGGATTGTCCTGGTCATAGTTCTTATCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA linear
, *** SEQUENCING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC119084 194929 bp DN.
Rattus norvegicus clone CH230-112G1,
                                                                                                                                                                                                                                                                                                               Db 16969 YKSMSYSKCYSRWMWCMSYYYCWGG 16945
                                                                                                                                                                                                                                                        848 CACCCAACACCCTTAGCTGCCCAGG
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                                                     Worley, K.C.
Direct Submission
Submitted (18-701-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jul 14, 2002 this sequence version replaced gi:20303396.
Center: Baylor College of Medicine
Center code: BCM
    Baylor College of Medicine, USA
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of Molecular and Human Genetics,
Baylor Plaza, Houston, TX 77030,
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Gaps

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214 AACCAGGCCAGGCAGTTGGTGTTGGAGTGAAGAGCAGACG-GCGGTGGGGAGGTCAGGA 272
                                                                                                                               273 GAGAATCTGCTGGGCTGGGGATGGTGTGGCCATCAACTGTCCCATTGCTGCAGGCTGGTC 332
94 CACCCCTTTGCCTCTGGCCTCACCCAGGCCCCCCAACCCCGCCCCCCAGCAGCTGTT 153
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"Human nuclear hormone receptor protein"
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Copyright (c) 1993 - 2003 Compugen Ltd.
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hormone receptor with a fully defined sequence of 457 amino acids given hormone receptor with a fully defined sequence of 457 amino acids given to the specification. The novel human unclear hormone receptor peptides and nucleic acids encoding them can be used as models for the development of human therapeutic targets, aid in the identification of therapeutic of human therapeutic serve as targets for the development of human therapeutic agents that modulate nuclear hormone receptor activity in cells and tissues that express the nuclear hormone receptor activity in cells and tissues that express the nuclear hormone receptor. The nucleic acids may be used as a query sequence to perform searches against sequence of primers, to construct recombinant vectors, to identify compounds that modulate nuclear hormone receptor nucleic acid expression, in gene therapy, and as antisense constructs to control nuclear hormone receptor can immune response, as a reagent in assays designed to determine protein levels in biological fluids, as markers for tissues in which a corresponding protein is expressed, to identify a binding partner/ligand to develop a system for the dentify compounds that modulate protein is dentify assays, and to identify compounds that modulate protein in development assays, and to identify compounds that modulate protein activity. This polynucleotide sequence represents the genomic DNA encoding the human protein assays.
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12799.13003
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10828..11004
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P-PSDB; AA021489.
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Length 20512;

DB 24;

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                                                                                                                                                                                                                                                                                                                                  ease; epilepsy; histone deacetylation; muscular dystrophy; single nucleotide polymorphism; SNP; cytosine methylation; iic; cytostatic; anticonvulsant; ds.
                 721 CCTAGGGAGGCATCCTCCATCCTTGGCCCTGGACAAGAAAATTGAACGTTGGTAGG
                                                            5720 CCTAGGGAGGCATCCTCATCCATCCTTGGCCCTGGACAAGAACTTGAACGTTGGTAGG
                                                                                     GGCCTCAGGACGATGCTGCGTGGCCCCTTGGGAATCTGGGATTGTCCTGGTCATAGTTCT
                                                                                                     5780 GGCCTCAGGACGATGCTGCGTGGCCCCTTGGGAATCTGGGATTGTCCTGGTCATAGTTCT
                                                                                                                                CCAGCCCTGTTCTGCCTACAGTGATGGGCATGGAGCCAGACACTGGGGAGGATTTGGCCA
                                                                                                                      841 TATCTIGCACCCAACACCCTIAGCIGCCCAGGCTTIGGACAIGGAIAGCCCCTACCCAAC
                                                                                                Human chemically modified disease associated gene SEQ ID NO 215.
                                                                                                                                                                                                    GTGAGGGCTGCCCTGCTGTGTGGGTCACCCCTCCTGGCTG 1001
                                                                                                                                                                                                                                                                                                                           diabetes;
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development genes, in particular disease related to homeobox containing genes (HOX), like diabetes, cancer, apoptosis related diseases, syndromes associated with congenital heart disease, epilepsy, diseases related to histone deacetylation, Currarino syndrome, diseases related with the development of the brain and limb girdle muscular dystrophy and dwarfism. Oligomers specific to each of the genes are useful for detecting the methylation state of all CPG dinucleotides within the 350 sequences or (II) and their complementary sequences, as primer oligonucleotides for the amplification of the 350 sequences, (II) and/or their complements and as oligomer probes for detecting the cytosine methylation state and/or single nucleotide polymorphisms (SNRs).

Note: The sequence data for this patent did not form part of the printed specification but it is based on sequence information supplied to berwent by
                                                                                                                                                                                                                                                                                                                                                                             AGTTTGGATTGTTTATTGTTATTGTTTTTACGTTTTGGAAAAAGTTAGTATAATAAAGGG 11778
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                                                                                                                                                                                                                                               Sequence 13508 BP; 2350 A; 286 C; 4030 G; 6841 T; 1 other;
                                                                                                                                                                                                                                                                           58.4%; Score 584.2; DB 24; Length
llarity 74.7%; Pred. No. 2.3e-152;
Conservative 0; Mismatches 248;, Indels
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Matches 733; Conserv
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The invention relates to a nucleic acid (I) comprising a sequence at least 18 bases in length of a segment of chemically pretreated DNA (II) of genes associated with development selected from 87 genes listed in the specification such as ACCPN, ADFN, or AFDI and comprising one of 350 sequences (ABN79984-ABN80333) or their complements. The invention is useful for the diagnosis or therapy of diseases associated with

Novel nucleic acid useful for diagnosis and therapy of diseases associated with development genes such as diabetes, comprises a sequence of a segment of chemically pretreated DNA of genes associated

WPI; 2002-130908/17

Claim 1; SEQ ID NO 215; 27pp; English.

with development

the printed to Derwent by

Length 13508;

other

6094 T;

.; G 3789 ပဲ 286

Sequence 13508 BP; 3338 A;

2222XX

single nucleotide polymorphisms (SNPs).
Note: The sequence data for this patent did not form part of the printe specification but is based on sequence information supplied to Derwent the European Patent Office.

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12559 TAGTIGITITAGGITITGGATATGGATAGTITITATITAATITAGTITIGITITGTTTATA 12618
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                                                                                                                                                                                                                                                                                                  Human; development; homeobox gene; HOX; diabetes; cancer; apoptosis; heart disease; epilepsy; histone deacetylation; muscular dystrophy; dwarfism; single nucleotide polymorphism; SNP; cytosine methylation; antidiabetic; cytostatic; anticonvulsant; ds.
TGGCCCCTTGGGAATCTGGGATTGTCCTGGTCATAGTTCTTATCTTGCACCCAACACCCT
                                         TAGCTGCCCAGGCTTTGGACATGGATAGCCCCTACCCAACCCAGCCCTGTTCTGCCTACA
                                                                                     GTGATGGGCATGGAGCCAGACACTGGGGAGGATTTGGCCCAGTGAGGGCTGCCCCTGCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel nucleic acid useful for diagnosis and therapy of diseases
                                                                                                                                                                                                                                                                             Human chemically modified disease associated gene SEQ ID NO
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ID ABN80199 standard; DNA; 13508
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2000DE-1043826
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                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                              AAAGTTAGCACAAAAAGGGCTGCTTTGTGGCTCACCCCCTCTGCCTCCTGGCCTCACCC
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 Score 507.2; DB 24; Length
Pred. No. 7e-131;
0; Mismatches 308; Indels
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Best Local Similarity 69.2%;
Matches 692; Conservative
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The invention relates to a nucleic acid (I) comprising a sequence at least 18 bases in length of a segment of chemically pretreated DNA (II) of genes associated with development selected from 87 genes listed in the specification such as ACCPN, ADFN. or AFD1 and comprising one of 350 sequences (ABN79984-ABN80333) or theat complements. The invention is useful for the diagnosis or therapy of diseases associated with cevelopment genes, in particular disease related to homeobox containing genes (HOX), like diabetes, cancer, apoptosis related diseases, syndromes associated with congenital heart disease, epilepsy, diseases related to histone deacetylation, curratino syndrome, diseases related with the development of the brain and limb glidle muscular dystrophy and dwarfism. Oligomers specific to each of the genes are useful for detecting the methylation state of all CpG dinucleotides within the 350 sequences or (II) and their complementary sequences, as primer oligonucleotides for the amplification of the 350 sequences, as primer oligonucleotides for the amplification of the 350 sequences, as primer ocuplements and so aligomer probes for detecting the cytosine methylation state and/or

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                                                                                                                                                                 Sequence encoding porcine C-type natriuretic peptide (CPN) precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genomic and cDNA encoding porcine CPN are claimed. Also claimed are fragments encoding the last 22 AAS (CPN-22) and the last 53 AAS (CPN-53). Proteins encoded are also claimed. The full lennyth DNA includes a promoter which may act in a brain-specific manner so could be used to control expression of other genes in the brain (see AAQ20465).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               246 GAGTICGAGGGACCTICGGCGGCGCTCCGGGCTICGGAGGGCCGGAGCGAGGGA 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         149 CTGTTCTCAGGCCTCTCAGC ---- CTGTCTGATTTGCTTGTCTGGCCTGGGGAGAATGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGTCAGGAGAGAATCTGCTGGGCTGGGGATGGTGGGCCATCAACTGTCCCATTGCTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTGGGAGAAAACCAGGCCAGGGCAGTTGGTGTTGGAGTGAAGAGCAGACGGCGGTGGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGCTGGTCTTGGGGCAGGGAAGGGGGATGGGGGGCCATAGCAGTGCTGGTCAGC 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding porcine C-natriuretic peptide - or precursor and fragments with natriuretic and hypotensive activities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 549;
                                                                                                                                                                                           Hypotensive agent; natriuretic; brain-specific promoter; ss
      Fuchimura K;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 549 BP; 85 A; 212 C; 178 G; 74 T; 0 other;
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Best Local Similarity 49.5%; Pred. No. 0.021;
Matches 145; Conservative 0; Mismatches 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Tanaka S,
                                                                                                                                                                                                                                            Location/Qualifiers
144..521
/*tag= a
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                                                                                    549
                                                                                                                                                                                                                                                                                                                                                                              90JP-0186583.
                                                                                                                                                                                                                                                                                                                                                     91EP-0111630
                                                                                                                                       (first entry)
                                                                                  AAQ20467 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Kangawa K,
                                                                                                                                                                                                                     Sus scrofa domestica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1992-017806/03.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; AAR20074
                                                                                                                                                                                                                                                                                                                                                    12-JUL-1991;
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                                                                                                                                       14-APR-1992
                                                                                                                                                                                                                                                                                                                           15-JAN-1992
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                                                                                                             AAQ20467
                                                          RESULT 5
AAQ20467/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CNP can be isolated from porcine brains using antibodies to CNP-22 (JA105047/90) and sequenced. The 22 and 53 C-terminal AAs have natriuretic and hypotensive activities, and are claimed (see AAR20182).
149 CTGTTCTCAGGCCTCTCAGC----CTGTCTGATTTGCTTGTCTGGCCTGGGGAAATGAG 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            246 GAGTTCGAGGGACCTTCGGCGCGCTCCGGGCTTGGCTTCGGAGGGCCCGGAGCGAGGAG 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      205 GIGGGAGAAAACCAGGCCAGGGCAGIIGGIGIIGGAGIGAAGAGCAGACGGCGGGGGGA 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       265 GGTCAGGAGAATCTGCTGGGCTGGGGATGGTGGGCATCAACTGTCCCATTGCTGCA 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            encoding porcine C-type natruiretic peptide (CNP) contg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              325 GGCTGGTCTTGGGGCAGGGAAGGGGATGGGGGGCCCATAGCAGTGCTGGTCAGC 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New C-type natriuretic peptide(s) isolated from porcine brain possess natriuretic and hypotensive activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 549;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.5%; Score 44.6; DB 13; Length
49.5%; Pred. No. 0.021;
tive 0; Mismatches 144; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 549 BP; 85 A; 212 C; 178 G; 74 T; 0 other;
                            961 GTGAGGGCTGCCCTGCTGTCTGGGTCACCCCTCCTGGCT 1000
                                           Natruiretic; hypotensive; hormone; ss
                                                                                                                                                                                                                                                                                             Location/Qualifiers
363..524
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minamino
                                                                                                                  AAQ20379 standard; cDNA; 549
                                                                                                                                                                                                                                                                                                                                                                                                      91EP-0111629
                                                                                                                                                                                                                                                                                                                                                                                                                               90JP-0186582
                                                                                                                                                                         (first entry)
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Matches 145; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1992-017805/03.
P-PSDB; AAR20182.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MATS/) MATSUO
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                                                                                                                                                                                                                 precursor
                                                                                                                                                                                                    Sequence
                                                                                                                                               AA020379
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The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db 187448 GCATCACTICAGGAICCCCGAGCAIGICGGCCAIGAGAICGAIGICAGCAGGCCGCIIGC 187507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel polynucleotides derived from Coryneform bacteria, for identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             615 GCCAGGAGCTGTGGGCACCTTTAAATGCCAGCCAGTCTCATGTGCCGGAGTTTGGGGTAG 674
       555 GCCCCAATTTTAGGGCCATGTGATTTGGGGCTATGTGACTCATGTCTGTAAGGTGCTTGG 614
                                                                                                                                                                                                                                                                                                                                                                                                                                  acid synthesis; vitamin; saccharide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 349980 BP; 79725 A; 90426 C; 98918 G; 80911 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mutant of coryneform bacterium, measuring expression amount and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO: 7062; 246pp + Sequence Listing; English.
                                                                                                                    162 GAGGGGGGGGGGGTTGGGGAGAGTGGGGGGGCAGTGGTTGTGGGGGGGAAA 110
                                                                           373 TCAGCCAGGCTGGCCTGGGAAGTGGTGCCCAGGCACTACTAAGAGCCAGGAAA
                                                                                                                                                                                                                                                                                                                                                                                    C glutamicum coding sequence fragment SEQ ID NO: 7062.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mizoguchi H, Ando S, Hayashi M,
Senoh A, Ikeda M, Ozaki A;
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Pred. No. 0.99;
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2000JP-0159162.
2000JP-0280988.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                Coryneform bacterium; amino organic acid synthesis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-DEC-2000; 2000EP-0127688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Corynebacterium glutamicum.
                                                                                                                                                                                                                                                                                                                                      (first entry)
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07-APR-2000;
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Fateishi N,
                                                                                                                                                                                                                                                                                        AAH68527;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating
                                                                                                                                                                                                                                                                                                                               Human; cytokine; cell proliferation; cell differentiation; gene therapy; accine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Note: The sequence data for this patent did not form part of the printer specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            193 GGGGAGAATGAGGTGGGAGAAAACCAGGCCAGGGCAGTTGGTGTTGGAGTGAAGAGCAGA 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         253 CGCCGGTGGGGAGGTCAGGAGAATCTGCTGGGCTGGGGATGGTGGGGCATCAACTGT 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   313 CCCATTGCTGCAGGCTGGTCTTGGGGCAGGGAAGGGGGATGGGGGGGCCATAGCAGTGCTGG 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 2027; 1399pp + Sequence Listing; English.
6 CGGAGCAGACTGGCCGGGCTGCTGCTGCGGGCGCGAGTCCCAGTGCTGCGGGGCGGG
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0; Mismatches 119;
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                                                                                                                                                                                                                                                                                   Human polynucleotide SEQ ID NO 2027
                                                                                                                                             ВР
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                                                                                                                    .967/c
AAI81967 standard; cDNA; 357
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18-MAY-2000; 2000US-0577409
                                                                                                                                                                                                                                       (first entry)
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     antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
Db 187508 GGCGGAAGCGGCGCGTTGGGTATTTGGCGGAGTCACTGGTTCAGCGTAGTTGCGGGGAG 187567
                                   DD 187568 GCCTCGGTCCAAAAGTTGGCTGAGGTTAGAGGTTGGTATCCGCCGGAACTCGGTGGAGTT 187627
                                                                                                                                                                                                                               Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
                                                                                                                                                                                                                                             immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer;
                       675 GGCTAGGTAGGATTGTGGAATATGGGAGGCAGGGATCTGTCTACCTAGGGAGGCATC 734
                                                                                                                                                                                                            Human nervous system related polynucleotide SEQ ID NO 9417
                                                                                        Db 187628 CAAGTTCAACGTGTGACGGGCGCAGAAGA 187656
                                                                 735 CTCATCCATCCTTGGCCCTGGACAAGAGA 763
                                                                                                                                            ABA17086 standard; DNA; 30032
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ABA17086
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316 ATTGCTGCAGGCTGGTCTTGGGGCAGGGGAAGGGGGATGGGGGGCCCATA 362
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                                                                                             RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention fetates to mover genes (manifold) and protecting or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification.

For isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, luver, luug, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune hyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and arasitic infections diseases such as viral, bacterial, fungal and antastic infections for this patent did not form part of the Note: The sequence data for this patent did not format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases -
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Human; immune; haematopoletic; immune/haematopoletic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                      Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38593.
Db 10168 GIGGGGACAGAAGGGGGTGTGGAAGACAGGAGGTGTGGGGGGACAGA 10214
                                     AAK83781/c
ID AAK83781 standard; DNA; 37664 BP
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2000US-0231968.
2000US-0232397.
2000US-023240.
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2000US-0233063.
2000US-0233064.
2000US-0233064.
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2000US-023423.
2000US-0234234.
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2000us-0237037.
2000us-0237038.
2000us-0237039.
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2000US-0246610.
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM8110 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynuclectides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent.

Clagnose and treat immune/haematopoletic related diseases, especially cancers and cancer metaatases of haematopoletic actived calls. AAK64703 to AAK87694 represent human immune/haematopoletic antigen genomic sequences from the present invention. AAK84950 and AAM82169 represent invention. AAK84951 to AAK84950 and AAM82169 represent invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DD: 15215 TTGGGGGGGGGGGGCCTGGAGGCGGGGGGGGGGGTGAATAGCAGCTGGAT 15156
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            195 GGAGAATGAGGTGGGAGAAACCAGGCCAGGTGGTGGTGGTGGAGTGAAGAGCAGACG 254
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                                                                                                                                                                                                                                                                                                                                                                            Ruben SM;
                                                                        200005-0250391.
200005-0251030.
200005-0251988.
200005-0251479.
200005-0251856.
                                                                                                                                                                                                               2000US-0251869.
2000US-0251989.
2000US-0251990.
2000US-0254097.
                                                                                                                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC
                                  2000US-0249300
2000US-0250160
                                                                                                                                                                                                                                                                                           05-JAN-2001; 2001US-0259678
                                                                                                                                                                                                                                                                                                                                                                          Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-483426/52
            17-NOV-2000)
17-NOV-2000)
10-DEC-2000)
10-DEC-2000)
10-DEC-2000)
10-DEC-2000)
10-DEC-2000)
10-DEC-2000)
10-DEC-2000)
10-DEC-2000)
11-DEC-2000)
                                                                                                                                                                                                                                                                                                                                                                          Rosen CA,
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AAK83782/c ID AAK83782 standard; DNA; 61710

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2000US-0249245
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                                                                                                                                        08-NOV-2000;
                                                                     02-051-2000)
02-051-2000)
02-051-2000)
02-051-2000)
13-051-2000)
20-051-2000)
20-051-2000)
20-051-2000)
20-051-2000)
20-051-2000)
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20-051-2000)
                                                                                                                                                                                                                                          17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                               17-NOV-2000;
                                          27-SEP-2000
 Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38594.
                             Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                  17-JAN-2001; 2001WO-US01354
                                                                                                                                                                                                                                                                                                         2000US-023239
            (first entry)
                                                 WO200157182-A2.
                                         Homo sapiens.
                                                                         31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
            07 - NOV - 2001
                                                                                                                                                                                                              22-AUG-2000;
                                                                                                                                                                                                                  -AUG-2000;
                                                          09-AUG-2001
   AAK83782;
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tiller production; delayed heading; gibberellic acid; phytohormone; golf; genetically modified grass; athletic field; sport; baseball; cricket; (obcball; rugby; soccer; tennis; lawn; landscaping; cattle; horse; sheep; goat; animal feedstuff; Arabidopsis thallana; Attl; homeobox gene; circular; cyclic; pVDH636.

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AAK54951.to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased complete, they may be used to treat disorders associated with decreased that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) colynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent.

C protein. (I) proteins and polynucleotides may be used to prevent.

C cancers and cancer metastases of haematopoietic-derived cells. AAK64703

C cancers and cancer metastases of haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK84950 and AAM82169

C represent sequences used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15325 GGTGAATGAGCAGCAGCCAGGCAGGCCAGGCCCTGGAGTTGAGTGGCAGCTGGGCAGAGC 15266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15205 TTGGGGGGGGGGGGCCTGGAGGCGGGCAGCCCTGGAGGTGAATACCAGCTGGTAT 15146
                                                                                                                                                                                                                                                                                                                    : acids encoding human immune/hematopoietic antigen polypeptides, for preventing, diagnosing and/or treating cancers and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           255 GCGGTGGGGAGGTCAGGAGAGAATCTGCTGGGCTGGGGATGGTGGCGATCAACTGTCC 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         195 GGAGAATGAGGTGGGAGAAAACCAGGCCAGGCCAGTTGGTGTTGGAGTGAAGAGCAGACG 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  315 CATTGCTGCAGGCTGGTCTTGGGGCAAGGGGATGGGGGGCCATAGCAGTGCTGGTC
                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 38594; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 61710 BP; 11560 A; 18542 C; 18148 G; 13460 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15145 GCCCGGGCAGGCCCTGGAGGTGAGGCAG 15116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transformation vector plasmid pVDH636 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        375 AGCCAGGCTGGCCTGGGAAGTGGTGCCCAG 404
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                   08-DEC-2000; 2000US-0251856.
08-DEC-2000; 2000US-0251868.
08-DEC-2000; 2000US-0251869.
08-DEC-2000; 2000US-0251990.
11-DEC-2000; 2000US-0251990.
05-JAN-2001; 2001US-0254097.
                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                        Ruben
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABK10687 standard; DNA; 9359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                      Barash SC,
                                                                                                                                                                                                                                                                              WPI; 2001-483426/52
                                                                                                                                                                                                                                                                                                                        Nucleic acids
                                                                                                                                                                                                                                                                                                                                                                  metastasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUN-2002
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ABK10687/c
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The invention relates to a grass plant which has been genetically modified to substantially inhibit generative propagation. The genetic modification may result in a heritable change in one or more plant characteristics such as inhibition of flowering (or substantial delay that amounts to inhibition), absence of inflorescence, increased production of tillers, delayed heading and inhibition of the developmental switch from vegetative to generative growth. A method of making a grass involves transforming the grass with a nucleic acid which interfers with metabolism of gibberalic acid. A grass can be treated by capplying a phytohormone to at least partially relieve or reverse a change in plant characteristic resulting from genetic modification. The genetically modified grass is useful for growing and/or propagating grass in athletic fields (for sports such as baseball, cricket, football, golf, rubpy, soccer and tennis), lawns, parks and other types of landscaping. The grass is also useful as an animal feedstuff for cattle, goats, horses and sheep, due to its increased vegetative growth, improved digestibility and/or nutritional value as animal feedstuff. This sequence represents plasmid publish pubmid publish bush. This plasmid was used as a transformation vector for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ij
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New genetically modified grass useful for growing and/or propagating grass in athletic fields (for sports such as baseball, cricket, football, golf, rugby, soccer and tennis), or as animal feedstuff for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 CCAGGCCCCCCAACCCCGCCCCCCAGCAGCTGTTCTCAGGCCTCTCAGCCTGTCTGATT 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         production of transgenic grasses expressing the Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       179 IGCTIGICIGGCCIGGGGAGAAIGAGGIGGGAGAAAACCAGGCCAGGGCAGIIGGIGIIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
4.1%; Score 41.4; DB 24; Length
Best Local Similarity 50.6%; Pred. No. 0.51;
Matches 119; Conservative 3; Mismatches 112; Indels
                                                                                                                                                                                                                                                                                                                                                                         /*tag= a
/product= "Arabidopsis thaliana AtHl"
                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Fig 6; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Van Der Valk P, Van Dun CMP,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-AUG-2000; 2000US-226422P.
27-NOV-2000; 2000US-253274P.
27-NOV-2000; 2000US-253327P.
22-JUN-2001; 2001US-300220P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-AUG-2001; 2001WO-EP09570.
                                                                                                                                                                                                                                                                                                                              4930..6351
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200214486-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-FEB-2002
                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                           Key
NAME OF THE PROPERTY OF THE PR
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12-JUL-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TATA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EP466175-A.
      in grasses
                                                                                                                                                                                                                                                                                                                     AAQ20466;
                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                     promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    promoter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a grass plant, which has been genetically modified to substantially inhibit generative propagation and carry herbicide resistance. The grass is useful for growth and/or propagation of grasses. The grass is used to play at least one sport (e.g. baseball, cricket, football, golf, rugby, soccer or tennis), or used at least in a portion of an athletic field, lawn or park. The grass is fed to animal (e.g. cattle, goat, horse or sheep) or used as animal feedstuff.

The present sequence represents the coding sequence of pVDH636 vector containing the Arabidopsis AtHI gene, which was used to inhibit flowering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New genetically modified grasses that express inhibited generative propagation, or herbicide resistance, useful for forage (e.g. cattle feedstuff) or amenity purposes (e.g. for use in an athletic field, lawn
                    GACTGAAGAGCAGCGGCGGGGGGGGCGTCAGGAGAATCTGCTGGGCTGGGGATGGTG 298
                                                                                                                                                                                                        PVDH636 vector; circular; cyclic; grass; plant; herbicide resistance; baseball; cricket; football; golf; rugby; soccer; tennis; lawn; park; athletic field; animal feedstuff; grass flowering inhibitor;
                                                        7236 TGGGVTTGCTATGGATGGTGGATAGCACTTTGGGGTTG 7182
                                            299 TGGGCATCAACTGTCCCATTGCT-GCAGGCTGGTCTTGGGGGCAGGGGAAGGGGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proveniers MCG;
                                                                                                                                                                                   eVDH636 vector containing Arabidopsis AtH1 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Smeekens SCM,
                                                                                                                                                                                                                                                                                                                                                                                                         /note= "No stop codon"
                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                          /*tag= a
/product= "AtH1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Fig 6; 56pp; English.
                                                                                                                      ABK11039 standard; DNA; 9359 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /an Der Valk P, Van Dun CMP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-AUG-2000; 2000US-226422P.
27-NOV-2000; 2000US-253274P.
27-NOV-2000; 2000US-253327P.
22-JUN-2001; 2001US-300220P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-AUG-2001; 2001WO-EP09572.
                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                     Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                              Oryza sativa.
Escherichia coli.
Cauliflower mosaic virus.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ADVA-) ADVANTA SEEDS BV.
                                                                                                                                                                                                                                                                                                                                                                                               partial
                                                                                                                                                                                                                                                              Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-257611/30.
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                                                                                                                                                                                                                                        AtH1; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                             WO200214524-A2.
                                                                                                                                                               05-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-FEB-2002
                                                                                                                                           ABK11039
                                                                                                                                                                                                                                                                          Sea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            park)
                                                                                                 RESULT 12
ABK11039/c
  239
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119 CCAGGCCCCCCAACCCCGCCCCCCAGCAGCTGTTCTCAGGCCTCTCAGCCTGTCTGATT 178
                                                                                                                                                                              239 GAGTGAAGAGCAGACGGCGGTGGGGAGGTCAGGAGAATCTGCTGGGCCTGGGGATGGTG 298
                                                                                                                                                                                                                                                                                                                                                          7236 TGGGVTTGCTATGGATCGTGGATAGCACTTTGGGCTTTAGGAACTTTAGGGGTTG 7182
                                                                                                                                                                                                                                                                                                                          TGGGCATCAACTGTCCCATTGCT-GCAGGCTGGTCTTGGGGCAGGGAAGGGGATG 352
                                     Length 9359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypotensive agent; natriuretic; brain-specific promoter; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fuchimura K;
Sequence 9359 BP; 2377 A; 2222 C; 2133 G; 2624 T; 3 other;
                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   promoter, for
                                   4.1%; Score 41.4; DB 24;
50.6%; Pred. No. 0.51;
ative 3; Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tanaka S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence of chromosomal gene, including pro C-type natriuretic peptide (CPN) precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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/note= "GC box"
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/label= Y box
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/*tag= b
/label= GC
100..105
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310..399
                                                    Best Local Similarity 50.6
Matches 119; Conservative
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P-PSDB; AAR20074.
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                                                                                                                                                                                                                                        322 GGRGRGGGGCATGGTGCTGTGGGGGGGGGGGCGCAGATCGGCGGCAGAGGTGCAC 263
                                                                                                                                                                                                                                                             295 GGTGTGGGCATCAACTGTCCCATTGCTGCAGGCTGGTCTTGGGGCAGGGAAGGGGATGGG 354
                                                                                                                                                                                                                                                                              262 GGGCCGGCGGGCAGACTGGCAAGCGAGCGGGAGCAGACTGGCCGGGCTGCGGTGCGGG 203
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                                                                                                                                                                                175 GATTTGCTTGTCTGGCCTGGGGAGAATGAGGTGGGAGAAAACCAGGCCAGGGCAGTTGGT 234
                                                                                                                                                               Gaps
                                                       are
                                               Genomic and cDNA encoding porcine CPN are claimed. Also claimed are fragments encoding the last 22 AAS (CPN-22) and the last 53 AAS (CPN-53). Proteins encoded are also claimed. The full length DNA includes a promoter which may act in a brain-specific manner so could be used to control expression of other genes in the brain
                                                                                                                                                                                                                                                                                                                                         415 GAGCCAGGAAAGCCCTGCCAAGGTTGTTGGCCTAGTTCCCTGTCATCAGCCGCC 468
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                                                                                                                                                                                                                                                                                                                                                      142 CGCCTTTATATCCAACCTGCCGCTGATGTCATCCTCCCGCCCACAAGGCCGCC 89
                                                                                                                                            Length 1894;
DNA encoding porcine C-natriuretic peptide - or precursor and fragments with natriuretic and hypotensive activities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C-type natriuretic peptide; CNP-22; CNP-53; hypotensive; ss
                                                                                                                                                              Indels
                                                                                                                     Sequence 1894 BP; 339 A; 614 C; 639 G; 302 T; 0 other;
                                                                                                                                          DB 13;
                                                                                                                                                   Pred. No. 0.87;
0; Mismatches 159;
                                                                                                                                  Score 39.6; DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Porcine C-type natriuretic peptide gene.
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complement (968..996)
/*tag= h
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                              Claim 13; Fig 3; 23pp; English
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/label= GC-box
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/label= GC-boc
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839..1129
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Best Local Similarity 45.9°
Matches 135; Conservative
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A chromosomal DNA fragment (AAT71220) includes the promoter region and structural gene coding for the precursor protein (AAW21990) of porcine C-type matriuretic peptides CNP-53 (AAW21991) and CNP-22 (AAW21992). It was isolated from a porcine chromosomal gene library using a probe prepd. by PCR amplification of porcine DNA using primers (see also AAT71222 and AAT71224) based on the N- and C-terminal portions of CNP-53. A signal peptide is present in the N-terminal region of the precursor protein (propro-CNP) and both CNP-22 and roll-53 are secreted when the structural gene is expressed in COS-1 colls. The structural gene is expressed in COS-1 for use in studying the biosynthesis and physiological actions of CNP and to develop pharmaceutical applications. The promoter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated porcine C-type natriuretic peptide gene - used to study the mechanisms of biosynthesis and physiological actions of CNP and to develop pharmaceutical applications
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Pred. No. 0.87;
0; Mismatches 159;
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/note= "primer KF225"
1088..1129
                                                                                      /note- "primer KF226"
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Best Local Similarity 45.9%;
Matches 135; Conservative
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Tawaragi Y;
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SUNR ) SUNTORY LID
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                           primer_bind
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200005-0231414.
200005-0232080.
200005-0232081.
200005-0231968.
200005-0232397.
200005-0232399.
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2000US-0232401.
2000US-0233063.
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08 - SEP - 2000; 09 - S
  Lung antigen protein; human; mouse; rabbit; goat; horse; cat; dog; chicken; sheep; immunosuppressive; antiarthritic; vasotropic; antihoumatic; antiproliferative; cytostatic; cardiant; neuroprotective; cerebroprotective; nottopic; antibacterial; virucide; fungicide; cancer; ophthalmological; vulnerary; gene therapy; autoimmune disease; neoplasm; hyperproliferative disorder; breast; liver; cardiovascular disorder; ds; cerebrovascular disorder; nervous system disorder; bacterial infection; fungal infection; viral infection; ocular disorder; endocrine disorder; gastrointesthal disorder; remal disorder; respiratory disorder; wound healing; skin aging; organ transplantation; food preservative; tissue regeneration; anti-infertility; food additive.
                                                   Human lung antigen genomic DNA #46
                                                                                                                                                                                                                                                                                                                                                      2000US-0180628.
2000US-0184664.
2000US-0186350.
2000US-0189874.
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20000S-0198123.
20000S-0205515.
20000S-0219467.
20000S-0215135.
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2000US-0224519.
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20000S-0225266.
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22-AUG-2000;
22-AUG-2000;
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14-AUG-2000;
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 AAS29976;
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Sequences AAS29931-AAS30164 represent genomic DNA molecules, which encode the lung antigen polypeptides of the invention. Lung antigen polypeptides are useful in the diagnosis, cand their associated polynuclectides are useful in the diagnosis, treatment and prevention of various types of disorders in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. A pathological condition can be determined by detecting the presence or absence of a mutation in a lung antigen polynucleotide. The treatable disorders include autoimmune diseases such as rheumatoid arthritis, hyperproliferative disorders such as neoplasms of the breast or liver, cardiovascular disorders such as cardiac arrest, cerebrovascular disorders such as cardiac arrest, cerebrovascular disorders such as corneal infection, endocrine disorders such as corneal infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Crohn's disease, renal disorders such as glomerulonephritis and also be used to aid wound healing, to prevent skin aging due to subburn, to maintain organs before transplantation, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated polypeptide for treating, preventing and/or prognosing respiratory disorders related to the lung including lung cancers and also for testing and detection e.g. diagnosis
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                                                                                                                                                                                                                                                                                                                                                                                                                        Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                             (HUMA-) HUMAN GENOME SCI INC.
                                                                                                       2000US-0251030
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05-JAN-2001;
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Search completed: March 30, 2003, 10:13:45 Job time : 670.299 secs

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Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 363, App Sequence 3, Appl Sequence 3, Appl Sequence 10, App Sequence 41, App Sequence 41, App Sequence 616, App Sequence 9833, Ap Sequence 29, Appl Sequence 3, Appl
             Sequence 346, App
Sequence 14, Appl
Sequence 7501, Ap
Sequence 202, App
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Sequence 136, App
Sequence 4563, Ap
                                                                     Sequence 20, Appl
Sequence 1, Appl1
Sequence 3, Appl1
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APPLICANT: Zhang,Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P4430R1C227
CURRENT APPLICATION NUMBER: US/10/184,644
CURRENT FILING DATE: 2002-06-28
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Sequence 20,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 312, Application US/10184644; Publication No. US20030044930A1
GENERAL INFORMATION: APPLICANT: Baker, Kevin P.
Watanabe, Colin K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
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Smith, Victoria
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; ORGANISM: HOMO
US-10-184-644-312
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Sequence 47, Appl
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Sequence 164, App
                                                                                           March 30, 2003, 13:12:08 ; Search time 75.7689 Seconds
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Sequence 5, Appli
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Sequence 20, Appl
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Sequence 261, App
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Sequence 240, App
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2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
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             GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-88-42-47
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194 LFLGQTGLGTTEEMGKLALEPGENFCMGGPGVIMSREVLRRAWPHIGKCLREMYTTHEDV 253
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                                                                                                                                                                                                     374 LEWEFLTGKYLYSAVDGQPPRRGMDSAQREALDDIVWQVMEMINANAKTRGRIDFKEIQ
                                            522 AGCCCCTGGTGTTCCCATGCTTCCTCTGTGCCCCCAATTTTAGGGCCATGTGATTTG
                                                                           254 EVGRCVRRFAGVOCVWSYEMROLFYENYEONKKGYIRDLHNSKIHQAITLHPNKNPPYQY
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Publication No. US20030054368A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA121C1
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Pred. No. 0.029;
0; Mismatches 88; Indels
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CURRENT FILING DATE: 2002-02-22
Prior Application removed - See File Wrapper or Palm: NUMBER OF SEO ID NOS: 428
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-764-878-240/c; Sequence 240, Application US/09764878; Patent No. US20020090615A1; GENERAL INFORMATION:
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51.1%;
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US-10-079-854;240/c
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TILEO PO INVENTION: Nucleic Acids, Proteins, and Antibodies.
FILE REFERENCE: PJ208
CURRENT APPLICATION NUMBER: US/09/989,442
CURRENT FILING DATE: 2001-11-21
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-00-34
PRIOR FILING DATE: 2000-05-04
PRIOR PLICATION NUMBER: 60/214,886
PRIOR PLICATION NUMBER: 60/214,886
PRIOR APPLICATION NUMBER: 60/217,487
PRIOR APPLICATION NUMBER: 60/217,487
PRIOR PLING DATE: 2000-06-18
PRIOR PELING DATE: 2000-06-18
PRIOR APPLICATION NUMBER: 60/217,487
PRIOR PILING DATE: 2000-06-11
                                         FILE REFERENCE: PA121
CURRENT APPLICATION NUMBER: US/09/764,878
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 428
SOFTWARE: Patentin Ver. 2.0
APPLICANT: Rosen et al. IIILE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
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Pred. No. 0.029;
0; Mismatches 88;
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FILING DATE: 2000-07-11
APPLICATION NUMBER: 60/225,447
FILING DATE: 2000-08-14
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FILING DATE: 2000-07-26
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APPLICATION NUMBER: 60/216,647
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APPLICATION NUMBER: 60/251,869
FILING DATE: 2000-12-08
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Publication No. US20030013649A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                          CRGANISM: Homo sapiens US-09-764-878-240
                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Thes 92; Conserva
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-09-989-442-47/C
                                                                                                                                                                                        SEQ ID NO 240
LENGTH: 5786
                                                                                                                                                                                                                                         TYPE: DNA
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NUMBER: 2000-09 NUMBER: 2000-09 NUMBER: 2000-09 NUMBER: 2000-09 NUMBER: 2000-08 NUMBER: 2000-0	NUMBER: 2000-10 NUMBER: 2000-11 2000-11 2000-11 2000-11 NUMBER: 2000-10 NUMBER: 2000-09 NUMBER: 2000-12	NUMBER: 2000-1 2000-1 2000-1 2000-0 NUMBER: 2000-0	2000-09 WUMBER: 2000-10 WUMBER: 2000-10 WUMBER: 2000-09 WUMBER: 2000-10
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R FILING DATE: 2000-08-14

R APPLICATION NUMBER: 60/235,836

RR APPLICATION NUMBER: 60/235,836

R APPLICATION NUMBER: 60/230,438

R FILING DATE: 2000-09-06

R FILING DATE: 2000-06-30

R APPLICATION NUMBER: 60/215,135

R RAPLICATION NUMBER: 60/225,266

R FILING DATE: 2000-08-14 R FILING DATE: 2000-11-08
R APPLICATION NUMBER: 66/246,532
R FILING DATE: 2000-11-08
R APPLICATION NUMBER: 66/249,216
R FILING DATE: 2000-11-17
R APPLICATION NUMBER: 60/249,210
R APPLICATION NUMBER: 60/226,681
R APPLICATION NUMBER: 60/226,681
R FILING DATE: 2000-08-22 R FILING DATE: 2000 11.77

R APPLICATION NUMBER: 60/249,244

R FILING DATE: 2000-11.17

R APPLICATION NUMBER: 60/249,217

R FILING DATE: 2000-11.17

R APPLICATION NUMBER: 60/249,211

R APPLICATION NUMBER: 60/249,212

R FILING DATE: 2000-11.17

R APPLICATION NUMBER: 60/249,215

R FILING DATE: 2000-11.17

R APPLICATION NUMBER: 60/249,214

R FILING DATE: 2000-11.17

R APPLICATION NUMBER: 60/249,297

R FILING DATE: 2000-11.17

R APPLICATION NUMBER: 60/249,297

R FILING DATE: 2000-11.17 R FILING DATE: 2000-08-14
R APPLICATION NUMBER: 60/225,213
R FILING DATE: 2000-08-14
R PILICATION NUMBER: 60/227,182
R FILING DATE: 2000-08-22
R APPLICATION NUMBER: 60/225,214 R FILING DATE: 2000-09-08
R APPLICATION NUMBER: 60/232,080
R FILING DATE: 2000-09-08
R PILING DATE: 2000-09-08
R FILING DATE: 2000-09-08
R APPLICATION NUMBER: 60/231,414 APPLICATION NUMBER: 60/249, 208 FILING DATE: 2000-11-17 APPLICATION NUMBER: 60/249, 213 FILING DATE: 2000-11-17 FILING DATE: 2000-09-14
APPLICATION WUMBER: 60/231,242
FILING DATE: 2000-09-08
APPLICATION NUMBER: 60/232,081 FILING DATE: 2000-11-17 APPLICATION NUMBER: 60/249,212 FILING DATE: 2000-11-17 FILING DATE: 2000-11-17 APPLICATION NUMBER: 60/249,207 APPLICATION NUMBER: 60/225,759 APPLICATION NUMBER: 60/249,218 APPLICATION NUMBER: 60/233,064 APPLICATION NUMBER: 60/233,063 2000-09-14 -60-000

Gaps

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Indels

Score 38.2; DB 10; Pred. No. 0.021; 0; Mismatches 66;

Length 246;

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70 ACAACAAAGGGCTGCTTTGTGGCTCACCCCTCTGCCTCTGGCCTCACCCAGGCCCCCC 129
                                                                                                                                                                     10 CTCCCCCCACCAGTCTGGATTGTTATTGTTACTGCTTTTACGTCTTGGAAAAAGTTAGC 69
                                                                                                                                                                                                        155 CIGCATGCCCANCIGCGAGIIGICITIIAACTIIGITIAITITIIAITINAAAAAAIG 96
                                                                                                                                                                                                                                                                        ; LOCATION: (245)
; OTHER INFORMATION: n equals a,t,g, or
US-09-783-590-7694
                                                                                                                                                                                                                                                                                                                             130 AACCCGCCCCCCCAGCAGCTG 151
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                                                                                             3.8%;
                                                                                                             Best_Local Similarity 53.5:
Matches 76; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Desnoyers, Luc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-184-644-164/c
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                                                                                          Query Match
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APPLICANT: ID11lon, Patrick J.

APPLICANT: ID11lon, Patrick J.

APPLICANT: Haseltine, William A.

APPLICANT: Haseltine, William A.

APPLICANT: Rosen, Craig A.

APPLICANT: Ruben, Steven M.

TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2

FILE REFERENCE: PO-16.2Cl

CURRENT FILING DATE: 1995-04-12

PRIOR FILING DATE: 1995-04-12

PRIOR APPLICATION NUMBER: 08/420,856

PRIOR FILING DATE: 1994-11-21

WUMBER OF SEQ ID NOS: 12485

SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    361 TAGCAGTGCTGGTCAGCCAGGCTGGCCTGGGAAGTGGTGCCCCAGGCACTACTAAGAGCCA 420
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                                                                                                                                                                                                                                                                                                                                         0; Mismatches
PRIOR APPLICATION NUMBER: 60/241,808
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/241,786
PRIOR APPLICATION NUMBER: 60/241,786
PRIOR APPLICATION NUMBER: 60/241,221
PRIOR PILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 60/231,243
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/231,243
PRIOR APPLICATION NUMBER: 60/231,243
PRIOR PILING DATE: 2000-09-08
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LOCATION: [(71)
OTHER INFORMATION: n equals a,t,g, or
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NAME/KEY: misc feature
LOCATION: (229)
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1 Similarity 51.1%;
90; Conservative (
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Matches
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1227 CURRENT APPLICATION NUMBER: US/10/184,644
CURRENT FILING DATE: 2002-06-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 GCACAACAAAGGGCTGCTTTGTGGCTCACCCCTTTGCCTCCTGGCCTCACCCAGGCCCC 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          233 SSM.HHYADWTM.D.SCDNDDYY.S.SDSYSYSYSYSSRACSYSYYNNRDYY.ADSYSYS 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
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Pred. No. 0.022;
99; Mismatches
Sequence 164, Application US/10184644 Publication No. US20030044930A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 33, Application US/09804682
Patent No. US20020106765A1
GENERAL INFORMATION:
APPLICANT: Kinders, Robert
                                                                                                                                                                                                                                                     Watanabe, Colin K.
Wood, William I.
                                                                                                                                                             Godowski, Paul J.
Gurney, Austin L.
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Best Local Similarity 4.88
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   224 GGGCAGTTGGTTGGAGTGAAGAGCAGACGGCGGTGGGGAGGTCAGGAGAATCTGCT 283
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LOCATION: (1999)..(3400)
OTHER INFORMATION: label - PRAC1, "promoter region of rice actin gene
OTHER INFORMATION: - contains an intron in the leader"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 14, 21, 27, 33, 36, 42, 72, 101, 103, 207, 208, 221, 223, LOCATION: 227, 235, 240, 242, 243, 247, 248, 259, 263, 265, 265, 278, LOCATION: 296, 321, 322, 324, 330, 332, 335, 336, 340, 367, 371, 385, LOCATION: 390, 393, 399, 401, 407, 415, 421, 447, 454, 471, 475 OTHER INFORMATION: n = A,T,C or G
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                                                                                                                              SAME AND METHODS FOR SCREENING FOR
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APPLICANT: COICEY, Michael J.
TITLE OF INVENTION: PAL-18 POLYPEPTIDES, NUCLEIC ACIDS
TITLE OF INVENTION: ENCODING THE SAME AND METHODS FOR
TITLE OF INVENTION: MODULATING THE SAME
FILE REFERENCE: 130001.406
CURRENT APPLICATION NUMBER: US/09/804,682
CURRENT FILING DATE: 2001-03-12
NUMBER OF SEQ ID NOS: 174
SOFTWARE: FastSEQ for Windows Version 4.0
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TITLE OF INVENTION: Improved Barstar Gene
FILE PEFERENCE: 2428-0108P
CURRENT APPLICATION NUMBER: US/09/970,921
CURRENT FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 4032
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: 14, 21, 27, 3
LOCATION: 227, 235, 24(
                                                                                                                                                                                                                                                                                                                                                                                                                              Q ID NO 33
LENGTH: 1065
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APPLICANT: WATNICK, Terry
APPLICANT: PHAKDEEKITCHAROEN, Bunyong
TITLE OF INVENTION: DEFECTION AND TREATMENT OF POLYCYSTIC KIDNEY DISEASE
FILE REFERENCE: JHU1680-2
CURRENT APPLICATION NUMBER: US/09/904,968A
CURRENT FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2000-07-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2664 TTTTTTTTTGCTGCGAGACGTGCGGTGCGGACAACTCACGGTGATAGTGGGGGGG 2605
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                                                                                             3'nos, "region containing 3' untranslated nopaline synthase gene of Agrobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240 AGTGAAGAGCAGACGGCGGTGGGGAAGTCAGGAGAATCTGCTGGGCTGGGGATGGTGT
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                                                                                                                                                                                                                                                                                                                                                                 Length 4032;
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US-09-904-968A-1/C
US-09-904-968A-1/C
Sequence 1, Application US/09904968A
Publication No. US20030008288A1
GENERAL INFORMATION:
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
                                                                                                                                                                                                                                                                                                                                                            Score 38; DB 10; Length 40
Pred. No. 0.063;
0; Mismatches 115; Indels
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                                                                                                                                                                                                                  Ncol, "Ncol recognition site,
                                                                                                                                                                                                                                                            COTHER INFORMATION: (4015)..(4021); CHER INFORMATION: label = KpnI, "KpnI recognition site" US-09-970-921-5
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                        barstar, "barstar DNA"
                                          NAME/KEY: misc_feature
LOCATION: (3577)...(4003)
OTHER INFORMATION: label = 3'n
OTHER INFORMATION: end of nop
OTHER INFORMATION: T-DNA"
NAME/KEY: misc_feature
LOCATION: (3399)..(3404)
OTHER INFORMATION: label = NC
                                                                                                                                                                                                                                                                                                                                                            3.8%;
ilarity 50.4%;
Conservative
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LOCATION: (3401)..(3676)
OTHER INFORMATION: label
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SOFTWARE: PatentIn version
                                                                                                                                                                                                                                          NAME/KEY: misc_feature
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Best Local Similarity
Matches 118; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 1
LENGTH: 53522
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                                                                                                                                                                APPLICANT: KINGER, Robert
APPLICANT: Corey, Michael J.
APPLICANT: Corey, Michael J.
TITLE OF INVENTION: PAL-18 POLYPEPTIDES, NUCLEIC ACIDS
TITLE OF INVENTION: MODULATING THE SAME
TITLE OF INVENTION: MODULATING THE SAME
CURRENT APPLICATION NUMBER: US/09/804,682
CURRENT APPLICATION NUMBER: US/09/804,682
KURRENT FILING DATE: 2001-03-12
NUMBER OF SEQ ID NOS: 174
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 1, 5, 7, 12, 13, 14, 15, 26, 39, 52, 87, 120, 121, 122, 123, LOCATION: 124, 125, 128, 130, 132, 133, 137, 141, 151, 152, 154, 160, LOCATION: 124, 174, 182, 184, 187, 189, 190, 192, 198, 200, 202, 202, 222, 225, 231, 233, 237, 238, 242, 246

OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           248 GCAGACGCCGGTGGGGAGGTCAGGAGAATCTGCTGGGGTTGGGGGATGGTGGGCATCA 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           188 GCCCTGGGGAGAATGAGGTGGGAGAAACCAGGCCAGGGCAGTTGGTGTTGGAGTGAAGA 247
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                                 Db 35536 GGGGGGGGGAAAGGAAGGAGGAAGGAGGAGGAGGGG 35498
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602,
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319 GCTGCAGGCTGGTCTTGGGGCAGGGGAAGGGGATGGGGGGG 357
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962,
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799,
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798,
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946,
                                                                                                                   Sequence 20, Application US/09804682
Patent No. US20020106765A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 462, 464, 473, 479, 484, LOCATION: 540, 543, 544, 555, 556, LOCATION: 579, 580, 582, 584, 589, LOCATION: 649, 650, 663, 665, 670, OTHER INFORMATION: n = A,T,C or G
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US-09-804-682-20
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LOCATION: 978, 980, 981
                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
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Best Local Similarity
Matches 90; Conserv
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LENGTH: 987
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Facent No. US20020099029A1
GENERAL INFORMATION:
GENERAL INFORMATION:
1 TITLE OF INVENTION: Induction of blood vessel formation through administration:
1 TITLE OF INVENTION: Polynuclectides encoding sphingosine kinases
1 TITLE OF THE REFERENCE: 4-31617
CURRENT PAPLICATION NUMBER: US/09/970,516
CURRENT PELLING DATE: 2001-10-04
NUMBER OF SEQ ID NOS: 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124 CCCCCCAACCCCGCCCCCCCAGCAGCTGTTCTCAGGCCTCTCAGCCTGTCTGATTTGCTT 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: POLYNGCLECTIONS ENCODING NOVEL SECRETED PROTEINS FILE REFERENCE: GIN 6400
CURRENT APPLICATION NUMBER: US/09/822,846
CURRENT FILING DATE: 2010.03-29
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                                                                                                                                                                                                     Agostino, Michael J.
Steininger II, Robert J.
Bowman, Michael R.
Spaulding, Vikki
Wong, Gordon G.
Application US/09822846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/195,605
PRIOR FILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 629
                                                                                                                                                                                                                                                                                                                                                                                                                      Graham, James R.
Genetics Institute, Inc.
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Patent No. US20020099029A1
                                                                                   McCoy, John M.
LaVallie, Edward R.
Collins-Racie, Lisa A.
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                     US20030027139A1
                                                                                                                                                                                                                                                                                                                                    Fechtel, Kim
Howes, Steven H.
                                                                                                                                                                 Merberg, David
Treacy, Maurice
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Matches 108; Conservative
                                                              APPLICANT: Jacobs, Kenneth
                                                                                                                                                                                                                                                                                                                 Clark, Hilary
                                                                                                                                             Evans, Cheryl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
Sequence 379, Applica Publication No. US200 GENERAL INFORMATION:
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US-09-970-516-3/c
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LENGIH: 993
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APPLICANT:
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PRIOR APPLICATION NUMBER: 60/259,434
                                                                                                                                                             ; Sequence 47, Application US/10032393; Publication No. US20030027286A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Vector pEPEF14
US-10-032-393-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 3.7%;
Best Local Similarity 46.9%;
Matches 114; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5370 CTT 5372
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APPLICANT: Spiegel, Sarah
APPLICANT: Spiegel, Sarah
APPLICANT: Spiegel, Sarah
APPLICANT: Kohama Takafumi
TITLE OF INVENTION: Mammalian Sphingosine Kinase Type 2 Isoforms, Cloning,
TITLE OF INVENTION: Expression and Methods of Use Thereof
FILE REPRENENCE: 00170/MG
CURRENT APPLICATION NUMBER: US/09/817,676A
CURRENT FILING DATE: 2001-03-26
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                              248 GCAGACGCGGTGGGGAGGTCAGGAGAATCTGCTGGGCTGGGGATGGTGTGGGCATCA 307
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55.0%; Pred. No. 0.11;
iive 0; Mismatches 75;
                                                                                                                                                                                                 DB 10;
                                                                                                                                                                                               Score 37; DB 1
Pred. No. 0.1;
0; Mismatches
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Patent No. US20020042101A1
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DATABASE ENTRY DATE: 2000-06-27
SOFTWARE: PatentIn version 3.1 SEQ ID NO 3
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Best Local Similarity 55.0%;
Matches 93; Conservative
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Best Local Similarity 55.0
Matches 93; Conservative
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NAME/KEY: CDS
LOCATION: (7)..(1860)
PUBLICATION, INFORMATION:
                               LENGTH: 1857
TYPE: DNA
ORGANISM: HOMO sapiens
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VOLUME: 275
                                                                                                      NAME/KEY: CDS
COCATION: (1)..(1857)
COTHER INFORMATION:
US-09-970-516-3
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PAGES: 19513-19520
DATE: 2000-06-30
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Pred. No. 0.26;
0; Mismatches 129; Indels 0;
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APPLICANT: Haselbeck, Robert

APPLICANT: Wall, Daniel

CURRENT APPLICATION NUMBER: US/10/032,393

CURRENT FILING DATE: 2001-12-21

PRIOR APPLICATION NUMBER: 60/259,434

PRIOR APPLICATION NUMBER: 60/269,434

PRIOR APPLICATION NUMBER: 60/2948,993

PRIOR PELING DATE: 2001-09-06

SPRIOR FILING DATE: 2001-09-06

SPRIOR FILING DATE: 2000-09-06

NUMBER OF SEQ ID NUSS: 68

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                         1099 GCTCCGACTTGGCACGAGGCAAGGCTATGGGCAGGGGTGGGCGAGGCAGG 1051
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APPLICANT: Haselbeck, Robert
APPLICANT: Wall, Daniel
APPLICANT: Gross, Molly
TITLE OF INVENTION: BACTERIAL PROMOTERS AND METHODS OF USE
FILE REFERENCE: ELITRA.010A
CURRENT APPLICALION NUMBER: US/10/032,393
CURRENT FILING DATE: 2001-12-21
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3.7%; Score 36.6; DB 9; Length 12739;
Best Local Similarity 46.9%; Pred. No. 0.26;
Matches 114; Conservative 0; Mismatches 129; Indels 0;
PRIOR FILING DATE: 2000-12-27
PRIOR APPLICATION NUMBER: 09/948,993
PRIOR FILING DATE: 2001-09-06
PRIOR PILING DATE: 2001-09-06
NUMBER OF SEQ ID NOS: 68
SOFTWARE: PASKSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 12739
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March 30, 2003, 08:06:43; Search time 1290.57 Seconds (without alignments) 12561.622 Million cell updates/sec
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

•	SUMMARIES	Ā	NS00397 AL063912 Drosophil	BH157536 . BH157536 ENTRL88TR	AG100622 B	BQ682356	ш	AL292445
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		n DB	-		-	٠.	٠.	-
		Length	1101					
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		Score	74	20	49.8	49.4	48.4	47.8
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please see http://www.fruitly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial

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ENTRL88TR Entamoeba histolytica Sheared DNA Entamoeba histolytica
EcoRI digestion of Drosophila DNA provided by the BDGP from the Isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Loftus, B., Wang, Z., Van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica
HM::MSS sheared DNA library (2001)
Unpublished (2001)
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                                                                                                                                 /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="BACR08A10"
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/db_xref="taxon:5759"
/clone_lib="Entamoceba histolytica Sheared DNA"
/clone_lib="Entamoceba histolytica Sheared DNA"
/clone_lib="Entamoceba histolytica Sheared DNA"
/note="voetor: phOS1; Site_l: Bst I; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica ausing a method described by Clark and Diamond (Clark, C.G., and Diamond, L.S. (1993) Entamoceba histolytica: a method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a tight size distribution (-2 kb). The v + 1 method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjloftus@tigr.org
Clones are derived from the Entamoeba histolytica HMI:IMSS sheared
DNA library
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Pan troglodytes DNA, clone: PTB-103E03.R, genomic survey sequence.
AG100622
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92 CTCACCCCTCTGCCTCCTGGCCTCACCCAGGCCCCCCAACCCCGGCCCCCCAAGCAGCTG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  212 AAAACCAGGCCAGGGCAGTTGGTTGGAGTGAAGAGCAGACGGCGGTGGGGAGGTCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                272 AGAGAATCTGCTGGGCTGGGGATGGTGTGGGCATCAACTGTCCCATTGCTGCAGGCTGGT
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                                                                                                                                                                                                                                                                                                                                                                                  /organism="Entamoeba histolytica"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pan troglodytes male lymphoblast DNA,
BAC Library clone:PTB-103E03.R.
Pan troglodytes
                                                                                                                                                                                                                                Seg primer: M13-Reverse
Class: shotgun
High quality sequence start: 68
High quality sequence stop: 206.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                         /strain="HM1: IMSS
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ORIGIN
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AG100622/c
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Submitted (02-AUG-2001) Asao Fujlyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suchiro-chou, Tsurumi - ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA linear EST 15-JUL-2002 sapiens cDNA clone IMAGE:6260920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1046)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                253 CGGCGGTGGGGAGGTCAGGAGAATCTGCTGGGCTGGGGATGGTGTGGCCATCAACTGT 312
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                                                                                      Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
 Taylor, T.D., Yada, T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 620
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2 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Male
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                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-103E03.R"
Fujiyama,A., Hattori,M., Toyoda,A.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee
365 c 97 q 96 +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    373 TCAGCCAGGCTGGCCTGGGAAGTGGTGCCCAGG 405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                            BAC end sequences of Library PTB
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                 : pKS145
                                                                                                                                                                                                                                                                                                                Sequencing: M13Rev
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                                                                                                                                                                                                                                                                              clone tracking errors.
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                                                                      (bases 1 to 620)
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R.Site 2
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AUTHORS
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cDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2420 row: m column: 17
High quality sequence stop: 231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             277 AICTGCTGGGCTGGGGATGGTGGGCATCAACTGTCCCATTGCTGCAGGCTGGTCTTGG
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                                                                                                                                                                                                                                                                                                                           /organism-"Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9606
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Submitted (12-APR-2000)
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis qenome. For more information, please take a look at http://www.genoscope.cns/fr/Tetraodon.
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                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Meopterygii; Teleostei; Buteleostei; Neoteleostei; Acanthomerpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.

1 (bases 1 to 817)
Rosst-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.
                                                                                                                                                                                                                                                                                                                                                    Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 817)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis Unpublished
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/clone_llb="G"
/note="Genoscope sequence ID : COBG112DD04LP1-end : T7"
/ 335 c 107 g 135 t 83 others
    Tetraodon nigroviridis genome survey sequence T7 end of clone 112HO8 of library G from Tetraodon nigroviridis, genomic survey
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/db_xref="taxon:99883"
/clone="112H08"
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4.8%; Score 47.8; DB 17;
Best Local Similarity 44.1%; Pred. No. 0.059;
Matches 123; Conservative 16; Mismatches 140;
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Tetraodon nigroviridis
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Edikaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 1398)

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: Gapbbs-rémail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution Information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.lln.gov

Plate: LLAM12140 row: 1 column: 21

High quality sequence stop: 225.
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                                                                                                                                                                                                BM479595 1198 bp mRNA linear EST 05-FEB-2002
AGENCOURT_6418829 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:5502428
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/clone_lib="NIH_MGC_67"
/tissue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
                                           757 CAAGAGAACTTGAACGTTGGTAGGGGCCTCAGGACGATG 795
                                                                    191 GCTAGGCTCGGGCTCGGGTCCTGACGTG 153
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Rax: 301 838 3543
Email: bjloftus@tigr.org
Clones are derived from the Entamoeba histolytica HMI:IMSS sheared
                                                                                                           Loftus, B., Wang, Z., Van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica
HMI:LMSS sheared DNA library (2001)
Unpublished (2001)
Contact: Brendan J Loftus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 TCTGCCTCCTGGCCTCACGCCCCCCAACCCCGCCCCCCAGCAGTGTTCTCAGGC 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    161 CTCTCAGCCTGTCTGATTTGCTTGTCTGGCCTGGGGAGAATGAGGTGGGAGAAAACCAGG 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 47.8; DB 17; Length 910;
Pred. No. 0.061;
0; Mismatches 157; Indels 0
                                                                                                                                                                                                                                                                                                                                                                            1. .910
/organism-"Entamoeba histolytica"
                                                                   Entamoeba histolýtica
Eukaryota; Entamoebidae; Entamoeba.
1 º(bases 1 to 910)
                                                                                                                                                                                                                                                                                                                                High quality sequence start: 7
High quality sequence stop: 319.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                         /strain="HM1:IMSS"
                         BH162948.1 GI:15736386
                                                                                                                                                                                                                                                                                                   Seq primer: M13-Reverse
genomic, DNA sequence.
                                                     Entamoeba histolytica
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Best Local Similarity 47.5%;
Matches 142; Conservative
                                                                                                                                                                                                                                                                                      ONA library
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KEYWORDS
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/d_xref="taxon:5759"
/done_lib="Entamoeba histolytica Sheared DNA"
/clone_lib="Entamoeba histolytica Sheared DNA"
/clone_lib="Vector: pHOS1; Site_l: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: method for isolate identification. Exp. Parasitol.
77:450.) The DNA was mechanically sheared to give a
tight size distribution (-2 kb). The v i imethod used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
                      BH157536 974 bp DNA linear GSS 24-SEP-2001
ENTRL88TR Entamoeba histolytica Sheared DNA Entamoeba histolytica
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: bjloftus@tigr.org
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
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                                                                                                                                                               Entamoeba histolytica.
Entamoeba histolytica
Eukaryota; Entamoebidae; Entamoeba.
1 (bases 1 to 974)
Loftus, B., Wang, Z:, Van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica
HM1: MSS sheared DNA library (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                               MD 20850,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Entamoeba histolytica"
/strain="HM1:IMSS"
                                                                                                                                                                                                                                                                                                                                                                                                                   The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0208
                                                                                                                                                                                                                                                                                                                                         Unpublished (2001)
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
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High quality sequence stop: 206.
Location/Qualifiers
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Seq primer: M13-Reverse
                                                                                                                       BH157536.1 GI:15730974
                                                                            genomic, DNA sequence.
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3H157536/c
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                                                                                                                                                                                                                                                                                   Lubrited (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - 'Web : www.genoscope.cns.fr)

- 'Web : www.genoscope.cns.fr)

- 'Web : www.genoscope.cns.fr)

- 'Gollaboration of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitily.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain vise for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be found at the provided by the can be
Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR13C17 of RPCI-98 library from Drosophila melanogaster (fruit AL065132
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                                                                                                                                                                         Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cound at http://bacpac.med.buffalo.edu/drosophila_bac.htm
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/db_xref="taxon:7227"
/clone="BACR13C17"
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Conservative 181; Mismatches
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/note="end : TET3"
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Best Local Simi
Matches 88;
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CNSO35G7 384 bp DNA linear GSS 15-MAY-2000 Tetraodon nigroviridis genome survey sequence T7 end of clone 213JO4 of library G from Tetraodon nigroviridis, genomic survey
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Tetraodon nigroviridis.
Tetraodon nigroviridis.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Meopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J. Human gene number estimate provided by genome wide analysis using Tetracoon nigroviridis DNA sequence
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Submitted (12-APR-2000)
This sequence is a single read and was generated as scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etded du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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/db_xref="taxon:7227"
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llarity 31.2%; Pred. No. 0.15;
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of a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                   CNSO1608 936 bp DNA linear GSS 26-JUL-19
Drosophila melanogaster genome survey sequence T7 end of BAC
BACN15N15 of DrosBAC library from Drosophila melanogaster (fruit
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila
1 (bases 1 to 936)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   188 GCCTGGGGAGAATGAGGTGGGAGAAAACCAGGCCAGGGCAGTTGGTGGTGGAGGA
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/db_xref="taxon:7227"
/clone="BACN15N15"
                    GGGATGGGGGCCCATAGCAGTGCTGGTCAGCCAGGCTGGCCTGGG
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); Mismatches 182;
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                                                                                                                                                                                                              fly), genomic survey sequence.
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                                                                                                                                                                                                                                                                                                         Drosophila melanogaster.
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311 c
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/Objection Note September / Colone | Note | 
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                                                                                                                                                                        Homo sapiens

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 951)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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Pan troglodytes DNA, clone: PTB-076M21.F, genomic survey sequence.
AG080593
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Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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      AL543262 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI001YC22
                                                                                                                                                                                                                                                                                                                                                                               Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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Totoki,Y., Watanabe,H. and Sakaki,Y.
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Matches 98; Conservative 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
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1. .951
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AL543262
AL543262.1 GI:12875740
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr

Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BAGs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazuctoyo Googawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2: cn bw sp, the same strain used for the BDGP's and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                           GSS 03-JUN-1999
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                                                                                                                                                      B84 bp DNA linear GSS 03-JUN-19 Drosophila melanogaster genome survey sequence T7 end of BAC # EACH4MAI of RPCI-98 library from Drosophila melanogaster (fruit AL065923
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                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Fullyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Toylor, Y. Watanabe, H. and Sakaki, Y. Direct Submission
Direct Submission
Submitted (02-A0G-2001) Asao Fuliyama, The Institute of Physical and Chemical Research (RIKBM), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
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Best Local Similarity 52.9%; Pred. No. 0.23;
Matches 90; Conservative 0; Mismatches 80; Indels 0

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Dikaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

I (bases 1 to 158766)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens chromosome 17, clone RP5-1112G21

Upublished

2 (bases 1 to 158766)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boquslavkiy, L., Boukhgalter, B., Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreitz, P., Filzhugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., McEwan, P., McGurk, A., McKernan, K., McCandor, T., O'Connor, T., O'Connor, T., O'Connor, T., O'Connor, T., O'Connor, T., O'Connor, T., Savery, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M., Wheeler, J., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M.
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20356. 20637
/rpt_danily="SINE/Alu"
/rpt_unit=AluSx
20955. .20992
/rpt_family="Simple_repeat"
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/rpt_unit=A-rich
complement(23861. .23963)
/rpt_family="LINE/L1"
/rpt_lamit=LINC4
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complement(20993. .21282)
/rpt_danily="SINE/Alu"
/rpt_unit=AluO
21956. .50413
/gene="TOP2A"
23401. .23438
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complement(25845. .26039)
/rpt_family="SINE/Alu"
/rpt_unit=AluSx
                                          .19264)
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/rpt_family="SINE/Alu"
.18607)
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/rpt_unit=AluX
complement(24884. .25201
/rpt_family="SINE/Alu"
/rpt_unit=AluSp
25268. .25554
                                                      /rpt_family="SINE/Alu"
/rpt_unit=Alusx
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/rpt_unit=AluYb8
                                            complement(18948.
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Direct Submission
Submitted (17-NOV-1999) Whitehead Institute/MIT Center for Genome Submitted (17-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Jul 8, 2001 this sequence version replaced 91:13123358.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                       ...... Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
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Sequencing vector: Plasmid; 108752; 48 of reads
Sequencing vector: Plasmid; 108752; 48 of reads
Chemistry: Dye-terminator Big Dye; 88 of reads
Chemistry: Dye-terminator Big Dye; 88 of reads
Chemistry: Dye-terminator Big Dye; 88 of reads
Consensus quality: 153948 bases at least Q40
Consensus quality: 15318 bases at least Q40
Consensus quality: 157160 bases at least Q20
Consensus quality: 157160 bases at least Q20
Consensus quality: 15786 bases at least Q20
Consensus quality: 15786 bases at least Q20
Consensus quality: 157866 s.

NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces
of 10 contigs. The true order of the pieces
at snot known and their order in this sequence record is a rubitrary. Gaps between the contigs are represented as a rubit ready will be updated with the finished sequence
as soon as it is available and the accession number will
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Center clone name: 112 G 21
Center clone namery Statistics
Sequencing vector: M13; M77815; 41% of reads
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of 1045 bp in length
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/note="assembly_fragment"
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4542: contig of
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                                                                                                                                                                                                                                                                       Length 158766;
                                                                                                                                                                                                                    914 others
                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                  ; Score 1001; DB 2;
; Pred. No. 5.3e-206;
0; Mismatches 0;
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38345 c 39366 g 42090 t
/note="assembly_fragment"
87324. 95421
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95522. 110722
/note="assembly_fragment"
110823. 124645
                                                                                               /note="assembly_fragment"
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156116. .158766
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                                                                                                                   124746. .156015
                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                       clone_end:T7
                                                                                                                                                                                                                                                                   Query Match
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JOURNAL REFERENCE AUTHORS

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6545 CCCAGGGAGACTGCAGCTGGGAGGGCTGGGTGAGGAGCGGGAGGACCTTCCTGG 6604
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 GGAAAGAGGAGGCAGAGCACCTAGGAGGGCACCGTCGCCTGGAGTGTGAGCTGGAGTAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 166368;
                                                                                                                                                                                                                                                                                                                                                      Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="RPCI-11 Human Male BAC"
39988 a 40877 c 42066 g 43337 t 100 others
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Web site: http://www-seq.wi.mit.edu
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Center clone name: 58_0_9
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Best Local Similarity 100.
Matches 1001; Conservative
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Submitted (14-DEC-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 166368)

Barra, N. Bastien, V. Bloom, T., Boukpalter, B., Barra, J., Chang, J., Chang, T., Boukpalter, B., Camarata, J., Chang, J., Chang, T., Boukpalter, B., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farfo, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gard, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLenn, C., Macdonald, P., Major, J., Matthews, C., Nacher, M., Meldrim, J., Meneus, L., Mihova, T., Mornan, C., Norman, C., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, D., Topham, K., Travers, M., Vassillev, H., P., L., Zimmer, A., and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC018629 166368 bp DNA linear HTG 19-AUG-2002 Homo sapiens chromosome 17 clone RP11-5809 map 17, *** SEQUENCING IN PROGRESS ***, 2 unordered pieces.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 '(bases 1 to 166368)
                                                                                          83384 GAAGGGGTGCCATGGAGAAGACCCTCACTCTCCCTCCTCCCCCAGAACAACAGCTCA 83443
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Homo sapiens chromosome 17, clone RP11-5809
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Direct Submission
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                                                     JOURNAL
                                                                                                       REFERENCE
                                                                                                                                         AUTHORS
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1 (pases 1 to 173441)
1 shran, B. , Nusbaum, C. and Lander, E. Homo sapiens chromosome 17, clone CTD-2267D19
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                                                                                                     541 CCTCTGCCAGCTGGGCAAATACACTACGGTATGGCTTTCCCCCGGCCTGCAGGGTGGGAT
                                                                                                                                                                                                                                                                                                                          721 AGCTCCCAGGAAGTGAAGGCTGGGTAGAGGCCAGGCCTGTGGGGGGCTGGAGCCAGGCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAACAACGTGTCTCTCTGGACATTGACCTCTGGGACAAGTTCAGTGAACTCTCCACCAAG
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481 GCCGGAGGTGGGGGAGCTCATTGAGAAGGTGCGCAAAGCGCACCAGGAAACCTTCCCTGC
                                                                                                                                                                                                                     TTGCCCAGGGCCACAGGGTGGGCCCCTCTCAGGCACCCTTCTTGTGCCAGGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (14-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 14, 2002 this sequence version replaced gi:22123315.
All repeats were idenced using RepeatMasKer:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasKer.html
                                                                            Submitted (24-SEP-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 3 (bases 1 to 173441)
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Web site: http://www-seq.wi.mit.edu
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Eukaryota; Metazoa; Chordata; Cran Mamanlai; Eutheria; Primates; Catal (Masses 1 to 1885/4) Birren, B., Nusbaum, C. and Lander, E. Homo sapiens chromosome 17, clone Unpublished 2 (bases 1 to 1885/4) Birren, B., Nusbaum, C., Lander, E., Barna, M., Bastlen, V.; Clang, J., Chararo, B., Cook, P., Cook, P., DeArellano, K., Gard, S., Gard, S., Graham, L., Grander, I., Hulme, W., Illev, I., Joh Horton, L., Hulme, W., Illev, I., McCarly, M. MacLean, C., Macdonald, P., Liu, G., MacLean, C., Macdonald, P., Schals, C., Landers, I., McCarthy, M., Meldrim, J., Meneus, I., Murphy, T., Naylor, J., Nguen, C., Noll, Phunkhang, P., Plerre, N., Raymond, C. Spencer, B., Stange-Thomm, K., Zhmer, A., Schauer, S., Teodore, J., Yopham, K., Zhmer, A., Green, P., (1996-199) http://ftp.genome.washington.edu/R. Center Globen Sate: http://www.seq.wi.mi Conter: Mitchead Institute/ M. Center clone name: 1029_L_16	Ď
REFERENCE AUTHORS TITLE JOURNAL COMMENT	FEATURES
1215 GGAAAGAGGCAGAGCACACAGGGCACCGTCGCCTCGAGTCTGAGCTCGACTACA (2116)	Db 71335 TGCATCATTAAGACTGGGGAGTTCGCCAAGCACTGCCGGCTTCACCACCTTCACCATC 71276 Qy 961 GCCGACCAGATCACCCTCCTCAAGGCTGCCTGCCTGCACT 1001

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aum, C., Lander, E., Ali, A., Allen, N., Anderson, S., en V., Bloom, T., Boyslavkly, L., Boukhgalter, B., en V., Bloom, T., Boyslavkly, L., Boukhgalter, B., P., Chazaro, B., Choepel, Y., Collymore, A., P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., ra, FitzGerald, M., Gage, D., Galagan, J., Graham, L., Grand-Pierre, N., Hagos, B., Garham, L., Johnson, R., Jones, C., Kamat, A., Is, C., Landers, T., Levine, R., Lindblad-Toh, K., C., Macdonald, P., Major, J., Matthews, C., Idrim, J., Meneus, L., Mihova, T., Mlenga, V., Or, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C. H., Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Ierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Schauer, S., Schupback, R., Seamen, S., Severy, P., Car, Stange-Thomann, N., Stojanovic, N., Talamas, J., Godore, J., Topham, K., Travers, M., Vassiliev, H., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J.,
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en, P. (1996-1997)
washington.edu/RM/RepeatWasker.html
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ead Institute/ MIT Center for Genome Research
IBR
Chordata; Craniata; Vertebrata; Euteleostomi;
Primates; Catarrhini; Hominidae; Homo.
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ummary Statistics
ector: Plasmid; n/4; 100% of reads
ector: Plasmid; n/4; 100% of reads
gram: Phrap; version 0.960731

ality: 186234 bases at least 0.30

ality: 187457 bases at least 0.30

ality: 187457 bases at least 0.20

187000; agarose-fp
1880074; sum-of-contigs
rage: 14.5 in Q20 bases; sum-of-contigs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ://www-seq.wi.mit.edu
nce_submissions@genome.wi.mit.edu
ject Information
name: L27554
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8: contig of 15350 bp in length
gap of 100 bp
0: contig of 39762 bp in length
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Direct Specer, B., Nusbaum, C., Lander, E., All, A., Allen, N., Anderson, S., Barren, B., Nusbaum, C., Lander, E., All, A., Allen, N., Anderson, S., Barren, N., Bastlen, V., Bloom, T., Bogulardkiy, L., Bouthgalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farceralra, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Grand-Pierre, M., Hagos, B., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Kartasa, A., Kells, C., Landers, T., Levine, R., Lindblad, Tch, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Mathews, C., Mcarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Nguyen, C., Nicol, B., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassillev, H., Direct Submission

AL Submitted (162-JUL-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 19030)

Shirten, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boukhallano, K., Diaz, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, P., Dearellano, K., Dearellano, K., Data, J., Changa, J., Chazaro, B., Choepel, Y., Changa, J., Charles, M., Cook, P., Dearellano, K., Data, J., Changa, J., Charles, P., FitzGerald, M., Gaqe, D., Galagan, J., Raratas, J., Karatas, J., Karatas, J., MacLean, C., Lander, F., Liu, Major, J., Mathhews, C., Lander, P., Liu, Gand-Plerre, N., Hajos, S., Karatas, J., MacLean, C., Macdonald, P., Major, J., Mathhews, C., McCarthy, M., Molsin, J., Meneus, L., Mihova, T., Meney, T., Meneus, T., Mangelan, C., Macdonald, P., Macd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo saplens chromosome 17 clone RP11-1029F16 map 17, WORKING DRAFT SEQUENCE, 11 ordered pieces.
                                                                                                 Db 155124 AGCTCCCAGGAAGTGAAGGCTGGGTAGAGGCCAGGCCTGTGGGGGGCTGGAGCCAGGCTGA 155065
                                                                                                                                                                                                 155064 GAAGGGGGCCATGGAGAAGGCCCTCACTCTCCCTCCCCCAGAACAACAACATCA 155005
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 190309)
                            155004 GAACAACGTGTCTCTGGACATTGACCTCTGGGACAAGTTCAGTGAACTCTCCACCAAG
                                                                                                                                                                         781 GAAGGGGTGCCATGGAGAAGAAGGCCCTCACTCTCCTCCTCCCCCAGAACAACAACTCA
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                                                                                                                                                                                                                                                                                                                                                                           TGCATCATTAAGACTGTGGAGTTCGCCAAGCAGCTGCCCGGCTTCACCACCCTCACCATC
                                                                             <u> AGCTCCCAGGAAGTGAAGGCTGGGTAGAGGGCCAGGCCTGTGGGGGCTGGAGCCAGGCTGA</u>
Birren, B., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 17, clone RP11-1029F16
Unpublished
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HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP
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ive 0; Mismatches 0;
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2173. .19348
/note="assembly_fragment"
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COMMENT

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Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Sman, J., Schauer, S., Schupback, R., Seaman, S., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Vola, R., Vola, R., Allson, B., Wu, X., Myman, D., Young, G., Zainoun, J., Direct Submission
                                                                                                                                                                                  NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Insert size: 179000; agarose-fp
Insert size: 189309; sum-of-contigs
Quality coverage: 15.5 in Q20 bases; sum-of-contigs
Quality coverage: 14.6 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: sequence_submissions@genome.wi.mit.edu
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66014: contig of 14544 bp in length
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contig of 42069 bp in length
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/clone_lib="RPCI-11 Human Male BAC"
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Pred. No. 5.2e-206;
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/note="assembly_fragment"
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31865. .33693
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Mus musculus chromosome 11 clone RP23-333D2, *** SEQUENCING
                                                                                                                                                                                                                                                                                                                    GAACAACGTGTCTCTCGGACATTGACCTCTGGGACAAGTTCAGTGAACTCTCCACCAAG
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        GGAAAGAGGAGGCAGAGCACCTAGGAGGCACCGTCGCCTGGAGTGTGAGCTGGAGTAGA
                                                                                                                            GCTGGAGTGCGTGGCAATGCCTTGCCTGCCCGTGAACGCGTGCTGTGTGCGCGTGCTTAC
                                                                                                                                                          AAGCCTGGGTGACCTCCTCAGCAGCTGGCAGCTCTCTGTCAGGCTGGGGGTGGACGAGGC
                                                                                                                                                                                         CCTGAGCAGCCTGCAGCTGCCCTCTTAACCCCCTCTGCCCTCCACACGTGAGAAACGA
                                                                                                                                                                                                                         CCGAAACAAGAAGAAGAAGGAGGTGCCCAAGCCCGAGTGCTCTGAGAGCTACACGCTGAC
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CCCAGGGAGACTGCAGCTGGGAGGCTGGGTGAGTGGAGGCGGGAGAAGGACCTTCCTGG
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AL591067
LOCUS
DEFINITION
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Hjalt, T.A. and Murray, J.C.
Genomic structure of the human retinoic acid receptor-alphal gene Mamm. Genome 10 (5), 528-529 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                           EMRB,
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                                                                                                                           TTGCCCAGGGCCACAGGGCCAGGATGGGCCCCTCTCAGGCACCCCTTCTTGTGCCAGGCA
                                AGCTCCCAGGAAGTGAAGGCTGGGTAGAGGCAGGCCTGTGGGGGCCTGGAGCCAGGCTGA
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                                                                                                                                                                                         Score 997.8; DB 9;
Pred. No. 4.7e-205;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 1233)
Hjalt,T.A. and Murray,J.C.
Direct Submitssion
Submitted (01-SPP-1998) Pediatrics,
Iowa City, IA 52242, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                               / 1. 1233
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="17"
/map="17q21.1"
/clone="BAC 205M17"
/gene="RARA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 235
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/gene="RARA"
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Homo sapiens
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                                                                                                                                                                                                                                Direct Submission
Submitted (30-JUL-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
hunquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
on Aug 11, 2002 this sequence version replaced gi:19848047.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db 148427 GAGGCACCCAAGCCCGAGTGCTCAGAGCTACACGCTGACCTGAGGTGGCGCGAGCTC 148486
                                                                                                                                              Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     440 GAGGTGCCCAAGCCCGAGTGCTCTGAGAGCTACACGCTGACGCCGGAGGTGGGGGAGCTC 499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator; 1% of reads
Chemistry: Dye-terminator Big Dye; 98% of reads
Consensus quality: 231046 bases at least Q40
Consensus quality: 231133 bases at least Q30
Consensus quality: 231138 bases at least Q20
Insert size: 231148; sum-of-contigs are passed to a least Q20
Consensus quality: 2358 error; agarose-fp
Quality coverage: 11.13x in Q20 bases; sum-of-contigs Quality
coverage: 11.16x in Q20 bases; agarose-fp
                                         AL591067.27 GI:22204212
HTG; HTGS_PHASEI; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            * NOTE: This is a 'working draft' sequence. It currently consists of 2 configs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as 'tuns of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 231248;
                                                                                                                                              Craniata; Vertebrata; E
Sciurognathi; Muridae;
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134202 134301: gap of 100 bp
134302 231248: contig of 96947 bp in length.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="assembly_fragment:07956"
56205 c 57206 g 62207 t
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134302. .231248
                                                                                                                                                                                                                                                                                                                                                                                                          Center code: SC
Web Site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Summary Statistics
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PROGRESS ***, 2 unordered pieces
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                                                                                                                                         Eukaryota, Metazoa, Chordata,
Mammalia, Butheria, Rodentia,
I, (bases 1 to 231248)
Lad, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /chromosome="11"
/clone="RP23-333D2"
/clone_lib="RPCI-23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center project name: bM333D2
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RS Murny, D. M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Banton, J., Binage, K., Blankenburg, K., Bonnin, D., Bonton, J., Bineva, M., Brown, E., Brown, M., Bryant, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, C., Coyle, M.D., Dathorne, S.R., David, R., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dunh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Farls, Y., Frantz, D., Fals, T., Ferragudo, D., Flago, N., Ford, J., Foster, P., Frantz, P., Falls, T., Ferragudo, D., Elago, N., Ford, J., Foster, P., Henrandez, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hornandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Kaatsovic, J., Kureshi, A., Lacier, A., Lucier, R., Lucier, A., Lucier, R., Lucier, R., Lucier, R., Lucier, Lucier,
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, *** SEQUENCING IN PROGRESS
DD 148487 ATTGAGAAGGTTCGCAAAGCGCACCAGGAGACCTTCCCGGCCCTCTGCCAGCTGGGCAAG 148546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db 148762 ACATTGACCTCTGGGACAAGTTCAGTGAACTCTCCACCAAGTGCATCATTAAGACTGTGG 148821
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Db 148642 CTGAGCAGAGGGGGAAAGGCAGCGAGCGGCCAGGCTGAAGCGGGTGCCAGTGCCGTAGCT 148701
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Rodentia; Sciurognathi; Muridae; Murinae;
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Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Mawhiney, E., McLeod, M. P., Meador, M., Mei, G., Metzker, M., Miner, G., Miner, Z., Mittchell, T., Mohabbatk, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newtson, N., Nguyen, A., Nguyen, N., Organ, M., Nguyen, N., Ordedo, R., Pace, A., Payton, B., Perery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pul, L. L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Primus, E., Pul, L. L., Quiles, M., Ren, Y., Scherer, S., Scott, G., Shen, H., Shocshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, R., Tansey, J., Taylor, C., Taylor, P., Talfrod, B., Thomas, N., Thomas, S., Ward-Moore, S., Warren, R., Washington, C., Walliams, G., Walliamson, A., Wleczyk, R., Wooden, S., Worley, K., Weinstock, G. and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTE: Estimated insert size may differ from sequence length : (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). NOTE: This is a "vorking draft' sequence. It currently consists of 72 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (19-FEB-2002) Human Genome Sequencing Center, Department
Of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 162393)
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Submitted (13-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jul 12, 2002 this sequence version replaced gi:18701588.
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Center clone name: GIA30-15011

Center clone name: GIA30-15011

Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 96609 bases at least Q40
Consensus quality: 105362 bases at least Q30
Consensus quality: 105362 bases at least Q20
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Web site: http://www.hgsc.bcm.tmc.edu/
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contig of 1108 b
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contig of 1719 b
gap of unknown l
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 50916] from the original journal article. This sequence comes from fig2b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   888 ACTCTCCACCAAGTGCATCATTAAGACTGTGGAGTTCGCCAAGCAGCTGCCCGGCTTCAC 947
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                                                                                                                                                                                                                                                                                                                                           Creating novel hematopoietic cell lines by expressing altered retinoic acid receptors.

Patent: 18, 5830766-45, 03-NOV-1998;
Location/Qualifiers
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de The,H., Lavau,C., Marchio,A., Chomienne,C., Degos,L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dejean,A.
The PML-RAR alpha fusion mRNA generated by the t(15;17
translocation in acute promyelocytic leukemia encodes
functionally altered RAR
Cell 66 (4), 675-684 (1991)
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100.0%; Pred. No. 2.7e-27;
iive 0; Mismatches 0;
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    1.1284
    7/gene="PML-RAR fusion gene"
    1.1251

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Sequence 5 from patent US 5830760,
AR052138
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/db_xref-"taxon:9606"
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Tsai, S. and Collins, S.J.
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S50916.1 GI:234248
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Matches 174; Conservative
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                                                                                                                                                                                                                                                    contig of 2040 bp in length gap of unknown length contig of 1826 bp in length gap of unknown length contig of 2602 bp in length contig of 2324 bp in length
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Pred. No. 3.8e-34;
                                   contig of 2603 b
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contig of 1742 b
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contig of 2363 b
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contig of 1444 b
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CHOTLIAICLICGDRQDLEQPDRVDMLQEPLLEALKVYVRKRRPSRPHMFPKMLMK
ITDLRSISAKGAERVTLKKEIPGSRPPLIQEMLENSEGLDTLSGQPGGGGRDGGGLA
PPPGSCSPSLSPSSNRSSPATHSP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AF242868 1572 bp mRNA linear SYN 24-APR-2000
Synthetic construct ECPP-retinoic acid receptor ligand binding
domain fusion protein mRNA, complete cds.
                                                                                                                                                                                     /translation="PNSNHVASGAGEAAIETQSSSSEEIVPSPPSPPPLPRIYRPCFV
CQDKSSGYHYGVSACEGGKGFFRRSIQKNMVYTCHRDKNCIINKVTRNRCQYCRLQKC
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artificial sequences.

1 (bases 1 to 1572)
Llopis.J., Westin,S., Ricote,M., Wang,J., Cho,C.Y., Kurokawa,R.,
Mullen,T.M., Rose,D.W., Rosenfeld,M.G., Tsien,R.Y. and Glass,C.K.
Ligand-dependent interactions of coactivators steroid receptor
coactivator-1 and peroxisome proliferator-activated receptor
binding protein with nuclear hormone receptors can be imaged in
live cells and are required for transcription
Proc. Natl. Acad. Sci. U.S.A. 97 (8), 4363-4368 (2000)
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Llopls,J., Westin,S., Ricote,M., Wang,J., Cho,C.Y., Kurokawa,R.,
Mullen,T.M., Rose,D.W., Rosenfeld,M.G., Tsien,R.Y. and Glass,C.K.
Direct Submission
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                   /note="This sequence comes from fig2b; conceptual translation presented here differs from translation in publication; RAR alpha"
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                                                                                                                 /product-"retinoic acid receptor alpha"
/protein_id-"AAB19602.2"
/db_xref-"G1:8815561"
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100.0%; Pred. No. 2.5e-27;
Live 0; Mismatches 0;
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/gene="PML-RAR fusion gene"
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/db_xref="taxon:9606"
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CTRYPPEDQITWTFSDGJTLNRTQMHAGRGPLTJLYFAFANQLLPLEMDDAETGLLSA
ICLIGGDRQDLEQPBYDMLQEPLLALLKVYRKRRSPRPHWPFKMLMKITDLRSISA
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PSPPPPLPRIXTRCPTVCREMSSGYHYGVSACESCKGFPRRSIGKNMYTCHRDKNCII
PNYTRANCOYCRLQFCEFVGASSGYHYGVSACESCKGFPRRSIGKNMYTCHRDKNCII
NYTRAHQETFPALCQLGKYTTNNSSEQRVSLDIDLMDKFSELSFKCIIKTVEFARQLFG
                                                                                                                                                       GIKAHFKIRHNIEDGSVQLADHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDH
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LKFICTTGKLPVPWPTLVTTLTMGVQCFSRYPDHMKQHDFFKSAMPBGYVQERTIFFK
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Petkovich, M., Brand, N.J., Krust, A. and Chambon, P. A human retinoic acid receptor which belongs to the family nuclear receptors
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Chambon,P.
Direct Submission
Submitted (22-DEC-1988)
cell line-MCF-7; library-lambda gt10; clone=p63.
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/note="retinoic acid receptor
/transl_table=11
/product="ECFP-retinoic acid
domain fusion protein"
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                                                    /protein_id="AAF65453.1"
/db_xref="G1:7638253"
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/db_xref="GI:35874"
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/organism="Homo sapiens"
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Human nucleophosmin-retinoic acid receptor alpha fusion protein
NPM-RAR short form mRNA, complete cds.
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Submitted (30-NOV-1995) Robert L. Redner, Medicine, University of
Pittsburgh, E1058 BST, 211 Lothrop Street, Pittsburgh, PA 15213,
USA
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/product="nucleophosmin-retinoic acid receptor alpha
fusion protein NPM-RAR short form"
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/tissue_type="bone marrow"
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/note="put. DNA-binding domain"
763. .764
/note="gc was cg in [1]"
/citation=[1]
824. .1483
/note="put. ligand-binding domain"
1396
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100.0%; Pred. No. 2.4e-27;
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/db_xref="taxon:9606"
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Submitted (04-JUL.2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan (E-mall:genomics@fri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) WEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Hellx Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RR, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and
/protein_id="AAB00113.1"
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Absortein_id="G1:1314310"
Aranslation="MEDSWIDMEDMSPLRPQNYLFGCELKADKDYHFKUDNDENBHQLSL"
ArvslgagakdeliveaeaannyegspikvtlatlkmsvQptvslggfelitppvvlrl
                                                                                                                 KCGSCPVHISGQHLVAIETQSSSSEEIVPSPPSPPPLPRIYRPCYCQDKSSGYHYGV
SACEGCKGFFRRSIQKNMVYTCHRDKNCIINKVTRNRCQYCRLQKCFEVGMSKESVRN
DRNKKKKEVPRPECSESYTLIPEVGELIEKVRKAHQETFPALCQLGKYTNNSSEQRV
                                                                                                                                                                                                  SLDIDLWDKFSELSTKCIIKTVEFAKOLPGFTTLTTADGITLLKAACLDILILRICTR
TYPEODTWFFSEDGLTLNRTQWINAGRYGPLTDLYPARANGLLPLEWDDAEFGLLSAICL
ICGDRODLEOPDRYDMLQPELLEALKYVYRRRPSRPHHFPKMLMKITDLRSISAKGA
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clone TRACH2015486, highly similar
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Shiohata,N., Matsumoto,K., Hirano,M., Sano,S., Nomura,R.,
Yoshikawa,Y., Matsumura,Y., Moriya,S., Chiba,E., Momiyama,H.,
Onogawa,S., Kacriyama,S., Satoh,N., Matsumawa,H., Takahashi,E.,
Rataoka,R., Kuga,N., Kuroda,A., Satoh,I., Kamata,K., Takahashi,E.,
Terashima,Y., Watanabe,M., Sugiyama,T., Irie,R., Otsuki,T.,
Sato,H., Ota,T., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y.,
Kawai-Hio,Y., Saito,K., Mishikawa,T., Kimura,K., Yamashita,H.,
Watsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K.,
Wagatsuma,M., Murakawa,R., Kawakami,B., Suzuki,Y., Sugano,S.,
Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.,
Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens trachea cDNA to mRNA, clone_lib:TRACH2
clone:TRACH2015486.
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100.0%; Pred. No. 2.4e-27;
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Isogai, T. and Yamamoto, J.
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Human PML/alpha-RA DNA encoding novel Nucleotide sequenc Human RARbeta2 PCR Human FLAG RARbeta Vector genome plas

ABK37492 ABK37493 ABK37494 ABK37495

AAQ19935 AAQ10388

AAQ20541 AAN90093 AAQ79934 AAT06491

AAS83048 AAF79992

AAS83

AAS83044

DNA encoding nove

Human liver RAR-be Encodes skin-speci Murine retinoic ac Mouse retinoic aci Mouse retinoic aci

Human Hap (hepatom Human liver hap cD

Human hepatoma ret

Human liver hap cD Clone pGEM-hRARgam Encodes human Reti

Human retinoic aci DNA encoding novel DNA encoding novel Human EST-derived

ALIGNMENTS

AAS81232 AAH98429

AAQ10389

"Human nuclear hormone receptor protein"

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/number= 1 1847..6808 684..1846

intron

Genomic DNA encod

Description

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AAT33247 AAT33260 AAS83808 AAS83045

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Result

AAS85136 AAS85135 AAL38338 AAS83049

17 23 23 24 24 24

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Genomic DNA encoding the human nuclear hormone receptor protein.
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New human nuclear hormone receptor proteins and nucleic acids, useful as models or targets for developing human therapeutic targets, and in identifying therapeutic proteins and modulators of nuclear hormone receptor expression.
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In the specification. The novel human nuclear hormone receptor with a fully defined sequence of 457 amino acids given in the specification. The novel human nuclear hormone receptor peptides and nucleic acids encoding them can be used as models for the development of human therapeutic targets, aid in the identification of therapeutic proteins, and serve as targets for the development of human therapeutic construct receptor activity in cells and tissues that express the nuclear hormone receptor activity in cells and telescent sequence to perform searches against sequence of databases to identify family members or related sequences, as probes or primers, to construct recombinant vectors, to identify compounds that modulate nuclear hormone receptor nucleic acid expression, in gene construct recombinant vectors, to identify compounds that the modulate nuclear hormone receptor nucleic acid expression, in gene expression in cells, tissues or organisms. The polypeptides can be used to raise antibodies or to elicit an immune response, as a reagent in assays designed to determine protein levels in biological fluids, as markers for tissues in which a corresponding protein is expressed, to identify a binding partner/ligand to develop a system for the clienting assays, and to identify compounds that modulate protein activity. This polymerication of inhibitors of the binding reaction, in drug screening assays, and to identify compounds that modulate protein activity. This control con
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                                            The invention relates to an isolated peptide of a
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Sequence 1481 BP; 308 A; 488 C; 425 G; 260 U; 0 other;
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10600 TIGCCCAGGGCCACAGGGCCAGGATGGGCCCCTCTCAGGCACCCCTTCTTGTGCCAGGCA 10659
                                           AGCTCCCAGGAAGTGAAGGCTGGGTAGAGGCCAGGCCTGTGGGGGGTTGAAGCCTGA 10779
                                                                                                                                                                  10900 TGCATCATTAAGACTGTGGAGTTCGCCAAGCAGCTGCCCGGCTTCACCACCTCACCATC 10959
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                                                                                            780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Retinoic acid receptor (RAR-alpha) RNA (AAT33247) is a substrate for ribozymes, external guide sequences and antisense oligonucleotides (see also AAT33245 and AAT33245-58) used for the treatment of acute promyelocytic leukaemia (APL). APL is characterised by a balanced, reciprocal translocation between the long arms of chromosomes 15 and 17, resulting in a fusion of the retinoic acid receptor gene (see also AAT33260) and a gene for a putative transcription factor, PML. The ribozymes etc. specifically cleave the PML-RAR-alpha fusion mRNA but not wild-type RAR-alpha mRNA.
                                                                                                                                                                                                                            RNA construct(s) including ribozyme(s) and antisense oligo:nucleotide(s) - for the inactivation of RNA associated with, e.g. promyelocytic leukaemia or follicular lymphoma
                                                                                         AGCTCCCAGGAAGTGAAGGCTGGGTAGAGGCCAGGCCTGTGGGGGGCTGGAGCCAGGCTGA
                                                                                                                                                    GAACAACGIGICICICICGACATIGACCICIGGGACAAGIICAGIGAACTICICACAAG
                                                                                                                                                                                                                                                                         TGCATCATTAAGACTGTGGAGTTCGCCAAGCAGCTGCCCGGCTTCACCACCCTCACCATC
                                                                                                       Hammerhead ribozyme; acute promyelocytic leukaemia; APL; lymphoma; therapy; PML-RAR-alpha; retinoic acid receptor; external guide sequence; EGS; antisense; ss.
                                                                                                                                                                                                                                                                                                                                                   GCCGACCAGATCACCCTCCTCAAGGCTGCCTGCCTGGACAT 1001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RAR-alpha RNA sequence.
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AAT33247
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Acute promyelocytic leukaemia (APL) is associated with a translocation between the long arms of chromosomes 15 and 17. resulting in the fusion between the retinoic caid receptor gene (RAR-alpha, AAT33260) and PML, a putative transcription factor gene. The fusion product RNA (see also AAT33246) junction region (AAT33251) is the target for ribozymes (AAT33245, AAT33248, AAT33250 and AAT33252), external guide sequences (AAT33253-54) and antisense constructs (AAT33255-57) that specifically cleave the PML-RAR-alpha fusion mRNA but not wild-type RAR-alpha mRNA (see also AAT33247).
                                                                                                                                                                                                                  828 GAACAACAGCTCAGAACAACGTGTCTCTCTGGACATTGACCTCTGGGACAAGTTCAGTGA 887
                                                                                                                       888 ACTCTCCACCAAGTGCATCATTAAGACTGTGGAGTTCGCCAAGCAGCTGCCCGGCTTCAC 947
                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hammerhead ribozyme; acute promyelocytic leukaemia; APL; lymphoma; therapy; PML-RAR-alpha; retinoic acid receptor; external guide sequence; EGS; antisense; ss.
                                                Indels
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; Score 174; DB 17;
; Pred. No. 6.1e-31;
35; Mismatches 0;
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Pred. No. 6.1e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RNA construct(s) including ribozyme(s) and oligo:nucleotide(s) - for the inactivation e.g. promyelocytic leukaemia or follicular
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100.0%; Pr⊷
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Query Match 17.4%;
Best Local Similarity 79.9%;
Matches 139; Conservative 3
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                 947
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                                                          New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
597 GAACAACACCTCAGAACAACGTGTCTCTCTGGACATTGACCTCTGGGACAAGTTCAGTGA
                                                                                                                                                                                                                              Sequence 1692 BP; 414 A; 470 C; 492 G; 316 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding novel human diagnostic protein #19612.
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The invention relates to isolated polynuclectide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chair reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in cappositics, forensics, gene mapping, identification of mutations candino acid sequences. AASK4197-AAS4954 represent novel human and and anno acid sequences. AASK4197-AAS4954 represent novel human
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                                                                                 828 GAACAACAGCTCAGAACAACGTGTCTCTCTGGACATTGACCTCTGGGACAAGTTCAGTGA 887
                                                                                                                      933 GAACAACAGCTCAGAACAACGTGTCTCTCTGGACATTGACCTCTGGGACAAGTTCAGTGA 992
                                                                                                                                                          888 ACTCTCCACCAAGTGCATCATTAAGACTGTGGAGTTCGCCAAGCAGCTGCCGGGCTTCAC 947
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                                               Indels
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           Score 174; DB 23;
Pred. No. 6.3e-31;
17.4%; Sco. 100.0%; Pred. No. 0, Mismatches
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2000US-0649167
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                                Similarity
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23-AUG-2000;
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                                                                                                                                                                          GAACAACAGCTCAGAACAACGTGTCTCTCTGGACATTGACCTCTGGGACAAGTTCAGTGA
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Note: The sequence data for this patent did not appear in the specification, but was obtained in electronic format directly at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                       Length 1944;
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                                                                    Sequence 1944 BP; 427 A; 598 C; 557 G; 362 T; 0 other;
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                                                                                                     Score 174; DB 23;
Pred. No. 6.5e-31;
                                                                                                                                         Mismatches
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23-AUG-2000; 2000US-0649167.
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                                                                                                                                       Conservative
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P-PSDB; ABG20949.
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The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human high grequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                      Length 1944;
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                                                                                                                                                         Sequence 1944 BP; 427 A; 598 C; 557 G; 362 T; 0 other;
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                                                                                                                                                                                      Score 174; DB 23;
Pred. No. 6.5e-31;
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2000US-0649167
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Matches 174; Conservative
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23-AUG-2000;
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to restore normal activity of (II) or to treat disease states involving (II) (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in disorders, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amin acid sequences. A&S64197-A&S94564 represent novel human call agreements of the invention.

Colagnostic coding sequences of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                      828 GAACAACAGCTCAGAACAACGTGTCTCTCGGACATTGACCTCTGGGACAAGTTCAGTGA 887
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                                                                                                                                                                                                                                                                                                          Sequence 2073 BP; 465 A; 612 C; 605 G; 391 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA encoding human nuclear hormone receptor protein.
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                                                                                                                                                                                                                                                                                                                                              Query Match
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In the specification in most manner in the second second second and nucleic acids encoding them can be used as models for the development of human therapeutic proteins, and serve as targets, aid in the identification of therapeutic of human therapeutic proteins, and serve as targets for the development of human therapeutic agents that modulate nuclear hormone receptor activity in cells and tissues that express the nuclear hormone receptor. The nucleic acids may be used as a query sequence to perform searches against sequence databases to identify family members or related sequences, as probes or primers, to construct recombinant vectors, to identify compounds that cherapy, and as antisense constructs to control nuclear hormone receptor nucleic acid expression, in gene expression in cells, tissues or organisms. The polypeptides can be used to raise antibodies or to elicit an immune response, as a reagent in assays designed to determine protein levels in biological fluids, as markers for tissues in which a corresponding protein is expressed, to identify a binding partner/ligand to develop a system for the identify campounds that modulate protein activity. This cassays, and to identify compounds that modulate protein activity. This polynucleotide sequence represents the cDNA encoding the human nuclear
                                                                                             The invention relates to an isolated peptide of a novel human nuclear hormone receptor with a fully defined sequence of 457 amino acids given in the specification. The novel human nuclear hormone receptor peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            860
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
Identifying therapeutic proteins and modulators of nuclear hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 2086;
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; Pred. No. 6.6e-31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hormone receptor protein of the invention.
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                                                         Claim 1; Fig 1; 73pp; English.
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2000US-0649167.
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                    receptor expression
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23-AUG-2000;
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828 GAACAACAGCTCAGAACAACGTGTCTCTGGACATTGACCTCTGGGACAAGTTCAGTGA 887
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          An RAR-alpha cDNA (given in AAQ81477) contained a truncation of sequences coding for the C-terminal 59 amino acids and part the 3' UTR of the wild-type human sequence (AAQ81476). This truncated cDNA, designated RAR-alpha-403, encoded a protein (AAR68024) containing the N-terminus, DNA-binding domain and part of the hormone-binding domain of RAR-alpha (AAR68023). RAR-alpha-403 has negative suppressor activity. Introduction into multipotent IL-3 dependent FDCP mix A4 cells (murine hematopoietic) caused a switch from neutrophil/monocyte differentiation to basophil/mast cells (30-50%), with only 2% neutrophils.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    888 ACTCTCCACCAAGTGCATCATTAAGACTGTGGAGTTCGCCAAGCAGCTGCCCGGCTTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New haematopoietic stem cell lines with specific differentiation properties - made by transfected stem cells with nucleic acid encoding dominant negative suppressor of the retinoic acid receptor alpha, useful e.g. for haematopoietic reconstitution
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   CDNA (AAQ81476) and insertion of s
TAG at deletion site (1312-1314)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2658 BP; 550 A; 889 C; 711 G; 508 T; 0 other;
                                                                                                                                                                                                                                                                                                                                    (HUTC-) HUTCHINSON CANCER RES CENT FRED.
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                                                                                                                                                                                                              28-JUL-1994;
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                                                                                             WO9504143-A.
                                                                                                                                                     09-FEB-1995.
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Best Local S
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                                                                                                                                                                                                                                                                                                                                          The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PECR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) and ists binding pariners are useful in medical imaging of sites expressing (II). (I) and ists binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are binding partners are useful for treating disorders involving aberrant protein expression or biological activity. (I peptide and polypeptide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and and continuous and sequences as AAS64454 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed continuous co
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                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID No 18853; 103pp; English
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Matches 174; Conservative
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                                                        WPI; 2001-639362/73.
P-PSDB; ABG18862.
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Drmanac RT,
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Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid; stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous; cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
792 ACTCTCCACCAAGTGCATCATTAAGACTGTGGAGTTCGCCAAGCAGCTGCCCGGCTTCAC 851
                                   Lung cancer related gene sequence SEQ ID NO:3551.
                                                                                                                                                                                ABL65214 standard; DNA; 2907 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         )2-OCT-2000;
                                                                                                                                                                                                                       ABL65214;
                                                                                                                                                                                                                                                                                                                                                                                                          gene; ds.
                                                                                                                                         RESULT 12
                                                                                                                                                             ABL65214
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                                                                                                                                                                                                     The invention relates to detecting (MI) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (Gs) identified by DNA chip analysis as given in the specification, and comparing the expression level to an expression level in an unactivated comparing the expression level to an expression of Gs is indicative of GCA.

Also included are medulating (M2) GA by contacting GC with an agent that alters the expression of at least one gene in Gs; (2) screening (M3) crownic) in a tissue, an altergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the chronic) in a tissue, an altergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the choic) in a tissue, an altergic response in a subject exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the the level of expression of the gene is indicative of inflammation; (4) treating (M5) an inflammation (especially chronic) or in a tissue, an altergic response in a subject, exposure of a subject to a pathogen or sterile inflammation (especially chronic) or in a tissue, an altergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by contacting a tissue having in the tissue, MI is useful for detecting GAN, M2 is useful for from GAN, M2 is useful for manial for firen GAN, M2 is useful for manial for firen GAN, M2 is useful for manial for manial for firen GAN, M2 is useful for manial for firen GAN, M2 is useful for manial 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease (e.g. psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, ARDS, adult respiratory distress syndrome, inflammatory bowel disease, Crohn's disease, ulcerative colitis, periodontal disease; also bacterial infection, viral infection, parasitic infection, protozoal infection, fungal infection and M5 is useful for treating one of the above conditions. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modulating GA; M3 is useful for screening an agent capable of modulating GCA preferably in an inflammation in a tissue; M4 is useful for detecting an inflammation (especially chronic) in a tissue, an allergic
                                                                                                                                                                                                                                                                                                                                          Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   828 GAACAACAGCTCAGAACAACGTGTCTCTGGGACATTGACCTCTGGGACAAGTTCAGTGA 887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        888 ACTCTCCACCAAGTGCATCATTAAGACTGTGGAGTTCGCCAAGCAGCTGCCCGGCTTCAC 947
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence represents a gene differentially expressed in granulocytes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formet directly from WIDO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17.4%; Score 174; DB 24; Length 2907; 100.0%; Pred. No. 7.1e-31; Live 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2907 BP; 561 A; 1011 C; 789 G; 546 T; 0 other;
                                                                                                                                                                                                                                                                 Vockley J;
                                                                                                                                                                                                                                                                 Yamaga S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID No 1088; 114pp; English.
                                                                                                                                                                                                                                                               Beazer-Barclay Y, Weissman SM,
                                                                                                                                                                                03-OCT-2000; 2000US-237189P.
                                                                                                                                         03-OCT-2001; 2001WO-US30821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 174; Conservative
                                                                                                                                                                                                                       (GENE-) GENE LOGIC INC.
                                                                                                                                                                                                                                                                                                    WPI; 2002-435328/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                          WO200228999-A2.
                                                                                                                                                                                                                                                                                                                                                                                                        drug toxicity
                      Homo sapiens.
                                                                                                   11-APR-2002
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Miller WH;

Young

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retinoic acid receptor (RAR) alpha gene. This gene is disrupted in a translocation of a portion of the long arm of chromosome 17 onto the long arm of chromosome 15 [f(15;17) (q21;q11-22)]. This causes a fusion between RAR-alpha and myl which is characteristic of acute promyelocytic leukemia (APL). The breakpoint region has been cloned and it has been shown that DNA rearrangements are clustered in the region of the first intron of RAR-alpha. This sequence was isolated by polymerase chain reaction (PCR). The primers used for amplification of this sequence can also be used to amplify the translocated region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                828 GAACAACAGCTCAGAACAACGTGTCTCTCTGGACATTGACCTCTGGGACAAGTTCAGTGA 887
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence given represents the nucleic acid sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fusion protein; myl; retinoic acid receptor-alpha; RAR; human; acute promyelocytic leukaemia; APL; t(15;17); translocation; treatment; all-trans retinoic acid; ss.
                                                                                                                                                                                                                                                                                Marker for acute promyelocytic leukaemia and other neoplasias comprising nucleic acid and encoded abnormal retinoic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2928 BP; 582 A; 1012 C; 789 G; 545 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note- "retinoic acid receptor-alpha"
                                                                                                                                                                   Kazizuka A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17.4%; Score 174; DB 13;
100.0%; Pred. No. 7.1e-31;
11ve 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 43-46; 84pp; English.
                                                                                                                                                                 Evans RM, Frankel S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= a
/product= "RAR-alpha"
                                                                                                                         (SLOK ) SLOAN KETTERING INST CANCER.
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                        92WO-US02320
                                                                91US-0673838
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Matches 174; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               103..1491
                                                                                                                                                                                                                                                                                                                           receptor-alpha receptor
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                                                                                                                                                                                                                        WPI; 1992-349240/42.
                                                                                                                                                                                                                                         P-PSDB; AAR27534
                                                                                                                                                                 Dmitrovsky E,
                                                             22-MAR-1991;
22-MAR-1991;
                        23-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sapiens
                                                                                                                                                                                     Warrell RP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                     The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL7010), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a structure and/or properties of the agent. MI can be used in the treatment of canneer such as socion, breast, stomach, lung, thyroid,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocaricationam, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's tumour.
                                           Horrigan S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            828 GAACAACAGCTCAGAACAACGTGTCTCTGGACATTGACCTCTGGGACAAGTTCAGTGA 887
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Retinoic acid receptor; RAR-alpha; myl; acute promyelocytic leukemia; APL; translocation; chromosome 17; chromosome 15; PCR; primer; [t(15:17)(q21;q11-22)]; breakpoint; polymerase chain reaction; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17.4%; Score 174; DB 24; Length 2907; 100.0%; Pred. No. 7.1e-31; tive 0; Mismatches 0; Indels 0;
                                         Endress G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2907 BP; 561 A; 1011 C; 789 G; 546 T; 0 other;
                                         Ebner R,
                                                                                                                                                                                                                Claim 1; SEQ ID 3551; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
103..1488
                                         Carter KC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAQ29338 standard; cDNA; 2928 BP
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                                         Augustus M,
                                                         Weaver 2;
(AVAL-) AVALON PHARM
                                                                                              WPI; 2002-188264/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RAR-alpha gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-MAR-1993
                                     Young PE, Soppet DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9216660-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Matches

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Gaps

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Length 2928; Indels

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828 GAACAACAGCTCAGAACAACGTGTCTCTCGGACATTGACCTCTGGGACAAGTTCAGTGA 887
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                                                                                                                                                                                    DNA of clone phRARI contg. the primary sequence of a protein (see corresp. AAP90395) that has ligand binding and transcription activating properties of retinoic acid receptor (RAR) protein. Used to make chimeric receptors, to produce receptor, to study binding complexes, and to screen cpds. for RAR-agonists and antagonists.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2940 BP; 594 A; 1010 C; 790 G; 546 T; 0 other;
                                                                                                        DNA encoding retinoic acid receptor proteins - used to produce proteins for studying complexes with ligands and in diagnostic assays.
                                                                                                                                                                                                                                                                                                        Query Match 17.4%; Score 174; DB 10; Best Local Similarity 100.0%; Pred. No. 7.1e-31; Matches 174; Conservative 0; Mismatches 0;
                                         Segui PS;
               (SALK ) SALK INST FOR BIOLOGICAL STUD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: March 30, 2003, 10:14:03 Job time : 214.299 secs
                                                                                                                                                              Disclosure; fig. 1B; 75pp; English.
                                        Ong ES,
                                        Evans RM, Giguere V,
                                                                 WPI; 1989-192701/26.
P-PSDB; AAP90395.
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                                                                                                                                                                                                                                                                           This sequence encodes the human retinoic acid receptor alpha, RAR-alpha which is used in a method for identifying a subject with acute promyelocytic leuksemia (APL) resulting from a t(15;17) translocation who will respond to treatment with all-trans retinoic acid. The protein can also be used to identify a subject with indications of APL who will not respond to treatment with all-trans retinoic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        851
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Diagnosis of acute promyelocytic leukaemia - by detecting nucleic acid encoding abnormal retinoic acid receptor-alpha
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                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
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                                                                                                                                             Dmitrovsky E, Frankel S, Miller WH, Warrell RP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clone phRAR1; DNA; retinoic acid receptor; ligand
                                                                                                                                                                                                                                                                                                                                                                                                   17.4%; Score 174; DB 20;
100.0%; Pred. No. 7.1e-31;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                  Disclosure; Column 29-34; 38pp; English.
                                                                                                                    (SLOK ) SLOAN KETTERING INST CANCER RES
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103..1449
/*tag= a
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                                                              93US-0095728.
91US-0673838.
91US-0675084.
                                     93US-0095728
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Matches 174; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
                                                                                                                                                                       WPI; 1999-044563/04.
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                                                                                                                                                                                     P-PSDB; AAW81964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complexes; human
                                                              21-JUL-1993;
22-MAR-1991;
                                    21-JUL-1993;
                                                                                         22-MAR-1991;
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           01-DEC-1998
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Length 2940; Indels

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                    GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-095-728B-1
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Sequence 5, Application US/08592383
Patent No. 5830760
GENERAL INFORMATION:
APPLICANT: TSA1, S. and S.J. Collins
TITLE OF INVENTION: "Hematopoletic Cell Lines Bearing Altered Retinoic Acid NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
DESCRIPTION: page 11; RAR-alpha RA binding region; positions 692 to 1395
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Pred. No. 4.3e-34;
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TELEPHONE: 1-206-682-8100; 1-206-224-0709(direct)
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Diskette-5.25 inch, 1.2Mb storage
US-08-649-619B-1
US-08-330-518-1
US-08-330-518-1
US-08-646-248-1
PCT-US95-13924-1
PCT-US95-13924-1
US-09-128-155-16
US-09-128-155-16
US-08-485-971-22
US-08-486-814-22
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US-08-162-184-22
US-08-162-184-22
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Mismatches
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SOFTWARE: WOR'D for Windows 5.01-t
COTREDY APPLICATION DATA:
APPLICATION NUMBER: US/08/592,383
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PRIOR APPLICATION DATA: 08/099,242
FILING DATE: July 28, 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17.4%; Sc..
100.0%; Pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 704 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
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GENERAL INFORMATION:
APPLICANT: DAITROYSKY, ETHAN
APPLICANT: WARRELL, JR, RAYMOND P
APPLICANT: MILLER JR, WILLSON H
APPLICANT: FRANKEL, STANLEY
TITLE OF INVENTION: TREATMENT OF ACUTE PROMYELOCYTIC LEUKEMIA (APL.)
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        828 GAACAACAGCTCAGAACAACGTGTCTCTCTGGACATTGACCTCTGGGACAAGTTCAGTGA 887
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/673,838
FILING DATE: 22 MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WHITE, JOHN P
REGISTRATION NUMBER: 38694-A
REFERENCE/DOCKET NUMBER: 38694-A
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTER/STICS:
LENGTH: 2928 base pairs
TYPE: nucleic acid
STRANDENESS: SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No.
                                                                                                                                                                                                                                                                ADDRESSEE: COOPER & DUNHAM LLP
STREET: 1185 AVENUE OF THE AMERICAS
CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/095,728B
FILING DATE: 21-JUL-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                      COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                      Sequence 3, Application US/08095728B Patent No. 5843642
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100.0%; Pr+
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Matches 174; Conservative
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                                                                                                                                                                                                                                                                                                                         NEW YORK
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PCT-US92-02320A-3
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                                     US-08-095-728B-3
                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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                                                                                                                                                                                                                                                                                                                 APPLICANT: TSAIN. S. and S.J. Collins
TITLE OF INVENTION: "Hematopoietic Cell Lines Bearing Altered Retinoic Acid Recept
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSE: Christensen, O'Connor, Johnson and Kindness
STREET: 2800 Pacific First Centre, 1420 Fifth Avenue
CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: cDNA to mRNA
DESCRIPTION: page 4,RAR-alpha403 dominant negative; deleted of 1311-1596 of SEO.
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888 ACTCTCCACCAAGTGCATCATTAAGACTGTGGAGTTCGCCAAGCAGCTGCCCGGCTTCAC 947
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION 135
PRIOR APPLICATION DATA
APPLICATION NUMBER: 08/099,242
FILING DATE: July 28, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Broderick, Thomas F.
REGISTRATION NUMBER: 31,332
REFERRICE/OCKET NUMBER: FHCR-1-7190
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION NOWER: FACR-1-7190
TELECOMMUNICATION NOWER: SHORY
TELECOMMUNICATION NO. 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette-5.25 inch, 1.2Mb storage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17.4%; Score 174; DB
100.0%; Pred. No. 6.6
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Word for Windows 5.01-t
CURRENT APPLICATION DATA: US/08/592,383
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC/386 Compatible OPERATING SYSTEM: MS-DOS 4.01
                                                                                                                                                                                                                                                              Sequence 3, Application US/08592383; Patent No. 5830760; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 174; Conservative
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STRANDEDNESS: double
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"Hematopoietic Cell Lines Bearing Altered Retinoic Aci
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                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/099,242
FILING DATE: July 28,1993
ATTORNEY/AGENT INFORMATION:
NAME: Broderick, Thomas F.
REGISTRATION NUMBER: 31,332
REFERENCE/DOCKET NUMBER: FHCR-1-7190
TELEPHONE: 1-206-682-8100; 1-206-224-0709(direct):
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2940 base pairs
TENETH : 2940 base pairs
TITLE OF INVENTION: "Hematopoietic Cell Lines Bearing R NUMBER OF SEQUENCES: 10
CORRESPONDENCES:
ADDRESSEE: Christensen, O'Connor, Johnson and Kindnes
STREET: 2800 Pacific First Centre, 1420 Fifth Avenue
CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TILLE OF INCENTION: RETINOIC ACID RECEPTOR COMPOSITION NUMBER OF SEQUENCES: 2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/546,256
FILING DATE: 06-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 276,536
FILING DATE: 30-NOV-1988
APPLICATION NUMBER: 128,331
FILING DATE: 02-DEC-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; APPLICANT: EVANS, RONALD M.;ONG, ESTELITA S.;SEGUI,;PRUDIMAR S.;THOMPSON, CATHERINE C.;UEMSONO, KAZUHIKO;GUGUERE, VINCENT
                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette-5.25 inch, 1.2mb storage COMPUTER: IBM PC/386 Compatible OPERATING SYSTEM: MS-DOS 4.01 SOFTWARE: Word for Windows 5.01-t CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 17.4%; Score 174; DB 2; 3
Best Local Similarity 100.0%; Pred. No. 6.8e-34;
Matches 174; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
DESCRIPTION: see Figure 16B; RAR-alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMMEDIATE SOURCE:
                                                                                                                                                         USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Patent No. 5171671
                                                                                                                                                  COUNTRY: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-592-383-1
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                                    APPLICANT: Sloan Rettering Institute, For Cancer Research
TITLE OF INVENTION: METHODS FOR DETECTION AND TREATMENT OF CANCER
NUMBER OF SEQUENCES: 6
GORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & DUNHAM
STREET: 30 ROCKEFELLER PLAZA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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6.8e-34;
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100.0%; Pred. No. 6.8
:ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.24 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US92/02320A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38694-PCT
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                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLIASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 675,084
FILING DATE: 22-MRR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 673,838
FILING DATE: 22-MRR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WHITE, JOHN P
REGISTRATION NUMBER: 38694-P
REGISTRATION NUMBER: 38694-P
RECENDENCE/DOCKET NUMBER: 38694-P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 644-0550
TELEFAX: (212) 644-0525
TELES: (212) 644-0525
TELEX: (212) 442023 GOOP UI
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 2928 base pairs
Sequence 3, Application PC/TUS9202320A
                                                                                                                                                                                                                                                                                                                             PC-DOS/MS-DOS
                                                                                                                                                                  CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10112
ZOMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATABLE
OPERATING SYSTEM: PC-DOS/MS-DC
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Patent No. 5830760
; General INFORMATION:
APPLICANT: Teal, S. and S.J. Co.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 174; Conservative
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EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: CDS
LOCATION: 103..1488
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IMMEDIATE SOURCE:
CLONE: hRAR ALPHA
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Best Local Similarity
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                      GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-592-383-1
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Gaps

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888 ACTCTCCACCAAGTGCATCATTAAGACTGTGGAGTTCGCCAAGCAGCTGCCCGGCTTCAC 947
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APPLICANT: MARRELL JR, RAYMOND P
APPLICANT: MILLER JR, WILSON H
APPLICANT: STANKEL, STANKER, STAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             888 ACTCTCCACCAAGTGCATCATTAAGACTGTGGAGTTCGCCAAGCAGGTGCCCGGCTTCAC 947
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                                                                                                                                                      1821 CACCCTCACCATCGCCGACCAGATCACCTCCTCAAGGCTGCCTGGACAT 1874
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Batentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/095,728B
FILING DATE: 21-JUL-1993
CLASSIFICATION: 435
PRIOR APPLICATION WASER: US 07/673,838
FILING DATE: 22-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WHITE, JOHN P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28,678
RFR: 38694-A
                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08095728B Patent No. 5843642
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 3869.
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3036 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Matches 174; Conservative
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ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
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US-08-095-728B-1
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CLONE: MYL-RAR
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CITY: NE
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APPLICANT: Calabretta, Bruno
APPLICANT: CASCISKI, Tomasz
TITLE OF INVENTION: ANTISENSE
TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
NUMBER OF, SEQUENCES: 55
CORRESPONDENCE ADDRESS:
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                                                                                              Length 2940;
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                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
                                                                                           Score 174; DB 6; Pred. No. 6.8e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.9e-34;
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                                                                        17.4%; Scott No. 0.100.0%; Pred. No. 0. 0. Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17.4%; Score 174; DB
100.0%; Pred. No. 6.9
:ive 0; Mismatches
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REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 8321-
TELEPHONE: (215) 568-8383
FELEPA: (215) 568-8383
FELEX: (215) 568-8383
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NAME: Monaco, Daniel A.
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TYPE: nucleic acid
                                                                                                                                              Conservative
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Matches 174; Conservative
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COMPUTER READABLE FORM:
                                                                                                                Best Local Similarity
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5171671-1
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                                                                                                                                           Matches 174;
                                                                                           Ouery Match
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                                                                                                                                               APPLICANT: Sloan-Kettering Institute, For Cancer Research
TITLE OF INVENTION: METHODS FOR DETECTION AND TREATMENT OF CANCER
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & DUNHAM
STREET: 30 ROCKEFELLER PLAZA
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Pred. No. 6.9e-34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 675,084
FILING DATE: 22-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 673,838
FILING DATE: 22-MAR-1991
ATTONNEY/AGENT INFORMATION:
NAME: WHITE, JOHN P
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/02320A
                                                                                                                 Sequence 1, Application PC/TUS9202320A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                     PC-DOS/MS-DOS
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100.0%; Pre
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 3869.
TELECOMMUNICATION INFORMATION:
TELEFRAM: (212) 977-9550
TELEFAX: (212) 644-0525
TELEX: (212) 42253 COOP UI INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                 : Floppy disk
IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 174; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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LOCATION: 67.2457

CTHER INFORMATION:

PCT-US92-02320A-1
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Best Local Similarity
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                                                                                                                                                                                                                                                   NEW YORK
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CLONE: MYL-RAR
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STRANDEDNESS:
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PCT-US92-02320A-1
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2236 ACTCTCCACCAAGTGCATCATTAAGACTGTGGAGTTCGCCAAGCAGCTGCCCGGCTTCAC 2295
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Pred. No. 7.2e-34;
0; Mismatches 0; Indels
Sequence 13, Application US/08892747

Patent No. 6057153
GENERAL INFORMATION:
APPLICANT: Shaji T. George, Michael Ma, Martina Werner,
APPLICANT: Umberto Pace and Allan R. Goldberg
TITLE OF INVENTION: Stabilized External Guide Sequences
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: 1..3511
OTHER INFORMATION: /function= "PML-RAR" DNA Sequence.
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                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/892,747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR PELITURI DATE:
FILING DATE: January 13, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US66/00513
FILING DATE: January 19, 1996
CLASSIFICATION: 435
ATTONNEY/AGENT INFORMATION:
NAME: PADST, PALEA L.
REGISTRATION NUMBER: 11,1109CIP2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                       ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 3511 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                             STATE: George
                                                                                                                                                                                                                                                                                   Georgia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
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                                                                                                COUNTRY:
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US-08-776-844-1
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                                                                                                                                                                                                                                                                                             822 CCCCCAGAACAACAGCTCAGAACAACGTGTCTCTCTGGACATTGACCTCTGGGACAAGTT 881
                                                                                                                                                                                                                                                                                                                            924 CACCACGAATICCAGIGCIGACCAICGAGICCGACIGGACCIGGGCCICIGGGACAAATI 983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      824 CCCAGAACAACAGCTCAGAACAACGTGTCTCTGGACATTGACCTCTGGGACAAGTTCA 883
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      882 CAGTGAACTCTCCACCAAGTGCATCATTAAGACTGTGGAGTTCGCCAAGCAGCTGCCCGG
             PPPLICANT: BLAUDIN DE THE, HUGHES; MARCHIO, AGNES; TIOLLAIS, PERRE; DEJEAN, ANNE STILLE OF INVENTION: STEROID/THYROID HORMONE RECEPTOR-RELATED PROTEIN INAPPROPRIATELY EXPRESSED IN HUMAN HEPATOCELLULAR CARCINOMA INMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: TAKAKU, FUMIMARO; ISHIKAWA, TAKASHI; IMAWARI, MICHIO; ;EVANS, ROMALD. M.; UMBESONO, KAZUHIKO; TITLE OF INVENTION: HUMAN GAMMA RETINOIC ACID RECEPTOR DNA NUMBER OF ; SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1576;
                                                                                                                                                                                                                               Length 2989;
                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                            0; Mismatches 42;
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                                                                                                                                                                                                                             DB 6;
                                                                                                                                                                                                                           Score 112.8; DB 6
Pred. No. 8.6e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 109.2; DB 6
Pred. No. 5.4e-18;
0; Mismatches 43
                                                                                             CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/134,130
FILING DATE: 17-DEC-1987

PRIOR APPLICATION DATA:

SEQ ID NO:1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/370,407
FILING DATE: 22-JUN-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
US-08-896-365-5
; Sequence 5, Application U$/08896365
; Patent No. 5939264
; GENERAL INFORMATION:
    APPLICANT: Rothschild, Max F.
; APPLICANT: Tuggle, Chrisopher K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.9%;
75.8%;
                                                                                                                                                                                                                           11.38;
76.78;
                                                                                                                                                                                                                                                             Conservative
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Best Local Similarity 75.8
Matches 135; Conservative
                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                              LENGTH: 2989
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;Patent No. 5260432
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5223606
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 ; Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5260432-1
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90 CACCACGAACTCCAGTGTAGACCACCGTGTGCAGCTGGATCTGGGGCCTGTGGGACCAAGT 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 822 CCCCCAGAACAACAGCTCAGAACAACGTGTCTCTGGACATTGACCTCTGGGA-CAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Messer, Lori A.
APPLICANT: Tun-Ping, Yu
TITLE OF INVENTION: GENES AND GENETIC MARKERS FOR IMPROVED
TITLE OF INVENTION: REPRODUCTIVE TRAITS IN ANIMALS
NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 558;
                                                                                                                                         ADDRESSEE: Zarley, McKee, Thomte, Voorhees & Sease
STREET: 801 Grand Avenue, Suite 3200
                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE PATENTIN STILL SOFTWARE PATENTIN STILL SOFTWARE PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/896,365 FILING DATE: US-015-1997 CLASSIFICATION: 435 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/022,180 FILING DATE: US-015-1996 ATTORNEY/AGENT INFORMATION:
NAME: Nebel, Headi S.
REGISTRATION NUMBER: 37,719 REFERENCE/DOCKET NUMBER: 15URF 021591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.7%; Score 86.6; DB 2; 74.2%; Pred. No. 1.4e-12;
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Embryo
                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 6277976
GENERAL INFORMATION:
APPLICANT: ENMARK, EVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 515-288-3667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      558 base pairs
nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 74.2
Matches 135; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   515-288-1338
                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
TISSUE TYPE: Embryo
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Search completed: March 30, 2003, 13:56:34
Job time: 45.7584 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   926 CCAAGCAGCTGCCCGGCTTCACCACCTCACCATCGCCGACCAGATCACCCTCCAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches · 50; Indels
APPLICANT: GUSTAFSSON, JAN
TITLE OF INVENTION: OR-1 ON ORPHAN RECEPTOR BELONGING
TITLE OF INVENTION: TO THE NUCLEAR RECEPTOR FAMILY
NUMBER OF SOUGHOUSE: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff
STREET: 1001 G Street, NW
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INC. 2010.
GENERAL INC. Shutsung
APPLICANT: LIAO, Shutsung
APPLICANT: LIAO, Shutsung
APPLICANT: SONG, Ching
TITLE OF INVENTION: UBIQUITOUS NUCLEAR RECEPTOR:
TITLE OF INVENTION: COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                  COMUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastEEG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,844
FILING DATE: 24-JUN-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/EP95/03247
FILING DATE: 16-AUG-1995
APPLICATION NUMBER: UK 9413536.2
FILING DATE: 16-AUG-1994
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 56; DB 4;
Pred. No. 7.7e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Kagan, Sarah A
REGISTRATION NUMBER: 32141
REFERENCE/DOCKET NUMBER: 00487.04029
TELECOMMUTCATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/08342411A Patent No. 5639616
                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1934 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 63.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid_
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-776-844-1
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US-08-342-411A-3
                                                                                                                                                                      STATE:
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866 ACCTCTGGGACAAGTTCAGTGAACTCTCCACCAAGTGCATCATTAAGACTGTGGAGTTCG 925
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Pred. No. 7.8e-05;
0; Mismatches 50; Indels
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/342,411A
FILING DATE: 18-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT
                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: KITCHELL, BARBARA S.
REGISTRATION NUMBER: 33,928
                                                                                                                                                                                                                                                                                                           TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1959 base pairs
                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 5.6%;
Best Local Similarity 63.2%;
Matches 86; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1118 CATCCACCATCGAGAT 1133
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS
256..1584
                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY:
; LOCATION:
US-08-342-411A-3
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us-09-691-220-3_copy_10000_11000.rnpb

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Sequence 524, Application US/09954456
Patent No. US20020115057A1
GENERAL INFORMATION:
APPLICART: Young, Paul
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents US:
FILE REFERENCE: 689230-76
CURRENT APPLICATION NUMBER: US/09/954,456
CURRENT FILING DATE: 2001-09-18
                                                                                                                                                     Sequence 12, Appl Sequence 16, Appl Sequence 22, Appl Sequence 22, Appl Sequence 202, Appl Sequence 202, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 21488, A Sequence 315, Appl Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3328, Apple Sequence 10, Apple Sequence 10, Apple Sequence 10, Apple Sequence 13861, Apple Sequence 13861, Apple Sequence 13804, Apple Sequence 13004, Apple Sequence 2304, Apple Sequence 23
                                                                                                    Sequence 17
Sequence 29
                             Sequence
                                                                          Seguence
                                                                                                                                                                                                                                                                         0 US-09-874-389-22

US-09-971-650-37

US-09-813-093-10

US-09-804-682-20

US-09-804-682-20

US-09-864-761-23488

US-09-864-761-675-20

US-09-864-761-675-20

US-09-80-107-3328

US-09-80-107-3328

US-10-044-090-316

US-09-80-107-3328

US-10-044-090-316

US-09-80-107-3328
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US-09-742-732-1
US-09-960-352-13861
US-09-880-107-3875
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US-09-864-761-2304
                                                                                             0 US-09-925-297-176
0 US-09-804-682-29
US-10-095-407-16
0 US-09-760-364-8
US-09-921-650-22
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PRIOR APPLICATION NUMBER: US/60/233,617
PRIOR PILING DATE: 2000-09-18
PRIOR PILING DATE: 2000-09-18
PRIOR PELICATION NUMBER: US/60/234,923
PRIOR PILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/235,134
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
PRIOR PILING DATE: 2000-09-25
PRIOR PILING DATE: 2000-09-26
PRIOR PILING DATE: 2000-09-26
PRIOR PILING DATE: 2000-09-26
PRIOR FILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 2276
NUMBER OF SEQ ID NOS: 2276
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US-09-954-456-524
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Sequence 5714, Ap
Sequence 2138, Ap
Sequence 12866, A
Sequence 7, Appli
Sequence 8, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 10, Appli
                                                                                                                                                                                                                                    March 30, 2003, 13:12:08; Search time 75.7689 Seconds (without alignments) 11242.392 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 cccagggagactgcagctgg.....aaggctgcctgcctggacat 1001
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/cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
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/cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
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/cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
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                                 GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-960-352-2138
US-09-960-352-12806
US-09-960-352-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                             US-09-691-220-3_COPY_10000_11000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        574371 seqs, 425486471 residues
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                                                                                                                                                                        nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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Perfect score:
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Gaps

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Length 2907; Indels

17.4%; Score 174; DB 10; 100.0%; Pred. No. 1.2e-38; 11ve 0; Mismatches 0;

Query Match 17.4 Best Local Similarity 100. Matches 174; Conservative

SOFTWARE: PatentIn version 3.0

SEQ ID NO 524 TYPE: DNA ORGANISM:

US-10-239-804-7 US-10-239-804-8 US-10-239-804-9 US-10-239-804-10 US-09-737-727-1

429 1375 1399 9127 9151 1577

US-09-833-381-92 US-09-909-446-1 US-09-909-325-1 US-09-909-326-1

456 1065

1117.6 1117.6 1117.6 1117.6 109.2 99.6 98.9 56 56 56 53.8

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Homo sapiens

US-09-954-456-524

Sequence 1, Appli Sequence 1210, Ap Sequence 92, Appl Sequence 33, Appl Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 567, App Sequence 1, Appli

US-09-962-436-567 US-10-013-823-1

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APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
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Clone ID: 10-LIB188-020-Q1-E1-C5
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Pred. No. 1.4e-36;
0; Mismatches 5;
                                       Score 166; DB 10;
Pred. No. 1.4e-36;
0; Mismatches 5
                                           DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECUM:
FILE REFERENCE: 15511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 12806, Application US/09960352
Patent No. US20020137139A1
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2138, Application US/09960352 Patent No. US20020137139A1
                                       Query Match
Best Local Similarity 97.1%;
Matches 169; Conservative
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Best Local Similarity 97.1%;
Matches 169; Conservative
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SEQ ID NO 2138
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ORGANISM: Bos taurus
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COTHER INFORMATION:
US-09-960-352-2138
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US-09-960-352-5714
                                       Query Match
Best Local
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APPLICANT:
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APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Magappan
TITLE OF INVENTION: NUCLEIC AGAPPAN
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REPERBNCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
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APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathalagan, Nagappan
APPLICANT: Mathalagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MISCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 5714
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                                                                                              ACTCTCCACCAAGTGCATCATTAAGACTGTGGAGTTCGCCAAGCAGCTGCCCGGCTTCAC 947
                                 828 GAACAACAGCTCAGAACAACGTGTCTCTCTGGACATTGACCTCTGGGACAAGTTCAGTGA 887
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA OGANISM: BOS taurus OTHER INFORMATION: Clone ID: 20-LIB188-012-01-E1-E11 US-09-960-352-4521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Clone ID: 25-LIB188-001-Q1-E1-G1
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Pred. No. 1.4e-36;
0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                 Sequence 4521, Application US/09960352
Patent No. US20020137139A1
PERERAL INFORMATION:
APPLICANT: Warren, Wesley C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5714, Application US/09960352
Patent No. US20020137139A1
PERERAL INFORMATION:
APPLICANT: Warren, Wesley C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 97.1%;
Matches 169; Conservative
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US-09-960-352-4521
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US-09-960-352-5714
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OTHER INFORMATION: Description of Artificial Sequence: FLAG RARbeta2; OTHER INFORMATION: PCR product US-10-239-804-8
                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence: RARbeta2 PCR OTHER INFORMATION: product
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           882 CAGTGAACTCTCCACCAAGTGCATCATTAAGACTGTGGAGTTCGCCAAGCAGCTGCCCGG
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Pred. No. 3.9e-23;
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Pred. No. 4e-23;
0; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Kinggman, Alan J
APPLICANT: Maden, Malcolm
APPLICANT: Corcoran, Jonathan PT
TITLE OF INVENTION: Factor
FILE REFERENCE: P009156WOCTH
CURRENT APPLICATION NUMBER: US/10/239,804
CURRENT FILING DATE: 2002-09-23
PRIOR FILING DATE: 2000-03:30
PRIOR APPLICATION NUMBER: GB 0024300.6
PRIOR APPLICATION NUMBER: GB 0024300.6
                                                        FILE REFERENCE: P009156WOCTH
CURRENT APPLICATION NUMBER: US/10/239,804
CURRENT FILING DATE: 2002-09-23
PRIOR APPLICATION NUMBER: PCT/GB00/01211
PRIOR FILING DATE: 2000-03-30
PRIOR FILING DATE: 2000-01-04
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn Ver: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8, Application US/10239804
Publication No. US20030053991A1
GENERAL INFORMATION:
APPLICANT: Oxford Blomedica (UK) Limited
                         Maden, Malcolm
Corcoran, Jonathan PT
                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                             11.7%;
78.3%;
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Best Local Similarity 78.3%;
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         Kingsman,
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Matches 141; Conserv
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US-10-239-804-8
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                                                                                                                                                                                                                                                       SEQ ID NO 7
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APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Byati, John C.
APPLICANT: Wathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REPERRENCE: 16511.006/37.21(10298)C
CURRENT APPLICATION NUMBER: U5/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
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                                                                                                                                                                                                                                                                                                                                                                  888 ACTCTCCACCAAGTGCATCATTAAGACTGTGGAGTTCGCCAAGCAGCTGCCCGGCTTCAC 947
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                                                                                                                   ; TYPE: DNA ; ORGANISM: Bos taurus ; ORGANISM: Bos taurus ; OTHER INFORMATION: Clone ID: 55-LIB188-005-Q1-E1-F4 US-09-960-352-12806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) ORGANISM: Bos taurus
) OTHER INFORMATION: Clone ID: 01-LIB188-009-Q1-E1-A1
US-09-960-352-31
                                                                                                                                                                                                             Score 166; DB 10;
Pred. No. 1.4e-36;
0; Mismatches 5;
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Pred. No. 1.4e-36;
0; Mismatches 5;
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILLING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 12806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Oxford Biomedica (UK) Limited
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 6
US-09-960-352-31
Sequence 31, Application US/09960352
Patent No. US:0020137139A1
GENERAL INFORMATION:
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97.18;
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Best Local Similarity 97.1%;
Matches 169; Conservative
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Best Local Similarity 97.1
Matches 169; Conservative
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Best Local Similarity
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LENGTH: 429
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US-10-239-804-7
                                                                                                   LENGIH: 417
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US-10-239-804-10
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US-09-797-727-1
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SEQ ID NO 1
LENGTH: 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               882 CAGTGAACTCTCCACCAAGTGCATCATTAAGACTGTGGAGTTCGCCAAGCAGCTGCCCGG 941
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643 CACCACGAATTCCAGCGCTGACCACCGGGTCCGATTGGACTTGGGCCTCTGGGACAAATT 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence: ponY-RARbeta2; OTHER INFORMATION: vector genome plasmid US-10-239-804-9
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Pred. No. 5.3e-23;
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                                                                                                                                                                                                                                                                                                     APPLICANT: Oxford Biomedica (UK) Limited
APPLICANT: Kingsman, Alan J
APPLICANT: Kingsman, Alan J
APPLICANT: Maden, Malcolm
APPLICANT: Maden, Malcolm
APPLICANT: Gorcoran, Jonathan PT
TITLE OF INVENTION: Factor
FILE REFERENCE: R099156W0CTH
CURRENT APPLICATION NUMBER: US/10/239,804
CURRENT FILING DATE: 2002-09-23
PRIOR FILING DATE: 2000-03-30
PRIOR FILING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 73
SOFTWARE: Patentin Ver: 2.1
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PRIOR FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: GB 0024300.6
PRIOR FILING DATE: 2000-10-04
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Publication No. US20030053991A1
GENERAL INFORMATION:
APPLICANT: Oxford Biomedica (UK) Limited
                                                                                                                                                                                                                                             Sequence 9, Application US/10239804 Publication No. US20030053991A1 GENERAL INFORMATION:
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APPLICANT: Maden, Malcolm
APPLICANT: Corcoran, Jonathan PT
TITLE OF INVENTION: Factor
FILE REFERENCE: P009156WOCTH
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Best Local Similarity 78.3%;
Matches 141; Conservative
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US-10-239-804-10
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LENGTH: 9127
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US-10-239-804-9
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3587 CTTCACAGGTCTGACCATCGCAGACCAGATCACCCTGCTCAAAGCCGCCTGCTTGGATAT 3646
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OTHER INFORMATION: Human Retinoic Acid Receptor-gamma (hRAR-gamma)
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                                                                                                                                                                                                                                                       Length 9151;
                                                                                                                                      FEATURE: OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: PONY-FLAG-RARbeta2 vector genome plasmid
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Pred. No. 8.4e 21;
0; Mismatches 43; 1
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FILLE REFERENCE: SALKILSO-3
CURRENT PAPLICATION NUMBER: US/09/797,727
CURRENT PAPLICATION NUMBER: US/09/797,727
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: US 08/486,325
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1990-06-22
PRIOR FILING DATE: 1990-06-22
PRIOR FILING DATE: 1989-06-22
                                                                                                                                                                                                                                                     11.7%; Score 117.6; DB 9;
78.3%; Pred. No. 5.3e-23;
11ve 0; Mismatches 39;
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Patent No. US20020077457A1
NUMBER OF SEQ ID NOS: 73
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 10
LENGTH: 9151
TYPE: DNA
ORGANISM: Artificial Sequence
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75.8%;
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Matches 141; Conservative
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Best Local Similarity 75.8
Matches 135; Conservative
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; LOCATION: (200)..(1576)
US-09-797-727-1
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                                                                                                                                                                                                                                                                             Similarity
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RESULT 14
US-09-804-682-33/c
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                                                                                             Sequence 1210, Application US/09833381

Patent No. U$20020132090A1

GENERAL INFORMATION:
APPLICANT: Robison, Keith E.
TITLE OF INVENTION: No. US20020132090Alel Nucleic Acid and Protein Homologs
FILE REFERENCE: 5800-119
CURRENT APPLICATION NUMBER: US/09/833,381
CURRENT FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 09/516,448
PRIOR FILING DATE: 2000-02-29
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TITLE OF INVENTION: No. US20020132090Alel Nucleic Acid and Protein Homologs
FILE REFERENCE: 5800-119
CURRENT APPLICATION NUMBER: US/09/833,381
CURRENT FILING DATE: 2001-04-11
PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 2050
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        829 AACAACAGCTCAGAACAACGTGTCTCTCTGGACATTGACCTCTGGGACAAGTTCAGTGAA 888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 CTCTCCNCCAAGTGCATNNTTAANACTGGGGAGTTCGCCAAGCAGTTGCCGG-TTTACN 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 10;
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Pred. No. 3.4e-18;
0; Mismatches 30
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0; Mismatches 10
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                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 2050
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1210
LENGTH: 848
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90.2%; Pred. No. 3
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                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (1)...(848)
COTHER INFORMATION: n = A,T,C or G
US-09-833-381-1210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 81.0%;
Matches 141; Conservative
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Best Local Similarity 90.23
Matches 129; Conservative
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                                                                              US-09-833-381-1210
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US-09-833-381-92/C
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                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
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Sequence 33, Application US/09804682

Petent No. US2020106765A1

GENERAL INFORMATION.

APPLICANT: Kinders, Robert

APPLICANT: Corey, Michael J.

TITLE OF INVENTION: PLI-18 POLYPEPTIDES, NUCLEIC ACIDS

TITLE OF INVENTION: ENCODING THE SAME AND METHODS FOR SCREENING FOR OR

TITLE OF INVENTION: MODULATING THE SAME

PILE REFERENCE: 130001.406

CURRENT APPLICATION UNMBER: US/09/804,682

CURRENT FILING DATE: 2001-03-12

NUMBER OF SEQ ID NOS: 174

SEQ ID NO 33

SEQ ID NO 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                65 AGAGGAGGCAGAGCACCTAGGAGGCACCGTCGCCTGGAGTGTGAGCTGGAGTAGACGCG 124
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923 TCGCCAAGCAGCTGCCCGGC-TTCACCACCTC-ACCATCGCCGACC--AGATCACCCTC
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Pred. No. 3.9e-06;
0; Mismatches 206; Indels
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; LOCATION: 842, 847, 888, 900, 909, 910, 916, 926, 927, 9
; LOCATION: 973, 1002, 1005, 1028, 1029, 1034, 1057, 1065
; CTHER INFORMATION: n = A,T,C or G
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822,
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LOCATION: 14, 21, 27, 33, 36, 42, 72, 101, 103,
LOCATION: 14, 21, 27, 33, 36, 42, 72, 101, 103,
LOCATION: 127, 235, 240, 242, 243, 247, 248, 25
LOCATION: 296, 321, 322, 324, 330, 332, 332,
LOCATION: 390, 393, 399, 401, 407, 415, 421, 44
OTHER INFORMATION: n = A.T.C or G
NAME/KEY: misc_feature
LOCATION: 479, 494, 501, 508, 511, 513, 525, 53
LOCATION: 721, 729, 735, 743, 747, 748, 754, 77
LOCATION: 721, 729, 735, 743, 747, 748, 754, 77
LOCATION: 721, 729, 735, 743, 747, 748, 754, 77
LOCATION: 721, 729, 735, 743, 747, 748, 754, 77
LOCATION: 721, 729, 735, 743, 747, 748, 754, 77
LOCATION: 721, 729, 735, 743, 747, 748, 754, 77
LOCATION: 721, 729, 735, 743, 747, 748, 754, 77
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LOCATION: 721, 729, 735, 743, 747, 748, 754, 77
LOCATION: 721, 729, 735, 743, 747, 748, 754, 77
LOCATION: 721, 729, 735, 743, 747, 748, 754, 77
LOCATION: 721, 729, 735, 743, 747, 748, 754, 77
LOCATION: 721, 722, 735, 743, 747, 748, 754, 77
LOCATION: 721, 722, 735, 743, 747, 748, 754, 77
LOCATION: 721, 722, 735, 743, 747, 748, 754, 77
                                                                                                                        979 CTCAAGGCTGCCTGCCTGGACAT 1001
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Best Local Similarity 44.5%;
Matches 167; Conservative
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ORGANISM: Homo sapiens
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Search completed: March 30, 2003, 16:46:16 Job time : 94.7689 secs

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APPLICANT: ENMARK, EVA
GUSTAFSSON, JAN
TITLE OF INVENTION: OR-1 ON ORPHAN RECEPTOR BELONGING
TO THE NUCLEAR RECEPTOR FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Kagan, Sarah A
REGISTRATION NUMBER: 32141
REFERENCE/DOCKET NUMBER: 00487.04029
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/909,446
FILING DATE: 19-Jul-2001
CLASSIFICATION: <a href="https://doi.org/10.1007/10.1007/">doi.org/10.1007/</a>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/776,844
FILING DATE: <URknown>
APPLICATION NUMBER: UK 9413536.2
FILING DATE: 16-AUG-1994
ATTORNEY/AGENT INFORMATION:
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MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-909-446-1
                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff
STREET: 1001 G Street, NW
CITY: Washington
STATE: DC
                                                                                                                                                                               Sequence 1, Application US/09909446 Patent No. US20020052489A1 GENERAL INFORMATION:
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LENGTH: 1934 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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INFORMATION FOR SEQ ID NO: 1:
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COMPUTER READABLE FORM:
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                                    365 AGCAGCCTGCAGCTG 379
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US-09-909-446-1
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BM817785 K-EST0084
BM790595 K-EST0070
BQ706025 AGENCOURT
BE794377 601589560
AL556392 AL556392
                                                                                     March 30, 2003, 08:06:43 ; Search time 1290.57 Seconds
    (without alignments)
    12561.622 Million cell updates/sec
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                          OM nucleic - nucleic search, using sw model
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gb_htc:*
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	DEFI	DEFINITION ACCESSION	MR4 -1 BI016	MR4-ET0138- BI016677	-190301-004-h0	-004	3	Homo sapiens cDNA,	DNA, mRNA	sednence.
	VERSION	ION	BIO1	6677.1	GI:14	:1442074	48			
	SOURC		human	n.						
	Š	ORGANISM	Euka1	Homo sapien: Eukaryota;]	Metazo	a;	::	Craniata; Vertebrata;	щ	.eostomi;
	REFE	RENCE	Mamm 1	malia; F (bases 1	Eutheri 1 to 63	а; 1)		=	Idae; Homo	ċ
	AU	AUTHORS	Dias Nagai Goldm	Netc , M.A.	IŲ.	cia lva, valh	R., Zag Mat	-ქტ	a, S., ., Cos G.S.,	
			M.J.	stein, A., ., Soares	res, F., I	live Bre	. 2.	Bucher, F., Jongeneel, ., Reis, L.F., de Souza	neel, C.V., Souza, S.J.	o'Hare and
	TIS	TITLE	Shote	yun sec	ncin	g of	the human	transcriptome w	with ORF ex	expressed
	105	JOURNAL MEDITARE	Proc.	Sequence to Proc. Natl.	l. Acad.	Sci	. U.S.A. 97	(7), 3491-3496	(2000)	
	COMMENT	ENT	Contact: Contact: Laborato Ludwig I	Contact: Si Contact: Si Laboratory Ludwig Inst	Contact: Simpson A.J. Laboratory of Cancer Ludwig Institute for	A.J.	.G. Genetics Cancer Research			
			Rua Pr Brazil	Prof. A	Antonio	Pru		andar, 01509-010,		Sao Paulo-SP,
			Tel:	55-11	1-2704922	22				
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21C Frontier Korean EST Project 2001
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Matches 174;
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                                                                                                                                                                                                                                                                       /note="Organ: lung_tumor; Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ij
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1 (bases 1 to 560)
Kim,N.S.; Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
              This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR4&t2=MR4-ET0138-190301-004-403&t3=2001-03-19&t4=1)
Seq primer: puc IB forward
High quality sequence stop: 551.
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Homo sapiens cDNA clone S21SNU520s1-2-F03
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160 c 229 g 128 t
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/organism="Homo sapiens"
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/clone_lib="ET0138"
/dev_stage="Adult"
  Email: asimpson@ludwig.org.br
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K-EST0084263 S21SNU520s1
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Best Local Similarity 98.7%;
Matches 376; Conservative
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BM817785
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Site_2: Noti; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including ECOR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of ECORI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Topolof' by electroporation method: The cDNA libraries constructed by this method are full-length enriched cDNA library. After analyzing and sequencing about 2,000 - 3,000 colonies in original cDNA library, the abundant cDNAs were selected and amplified by PCR reaction using vector region primer including T7 promotor as 5' primer and N(dT)44 as 3' primer. The PCR products were used as transfed RNA by in vitro transcription
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-"Organ: Stomach; Vector: pTZ18RP1; Site_1: EcoRI;
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                                                                                      Korea Research Institute of Bioscience & Biotechnology 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
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/cell_line="SNU-520"
/lab_host="Top10F'"
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Pred. No. 2.1e-29;
0; Mismatches 0;
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/clone_lib="S21SNU520s1"
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/organism="Homo sapiens"
                                                                                                                                                                                                                  Email: yongsung@mail.kribb.re.kr
Plate: 2 row: F column: 03
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187 c 160 g
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                                                                                                                                                  Tel: +82-42-860-4470
Fax: +82-42-860-4409
Unpublished (2002)
Contact: Kim YS
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BM790595 646 bp mRNA linear EST 05-MAR-2002
K-EST0070459 S21SNU520 Homo sapiens cDNA clone S21SNU520-11-G11 5',
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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1 (bases 1 to 646)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
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Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="Stomach"
/cell_type="Floating aggregates"
/cell_line="SNU-520"
/lab_host="roploF'"
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/clone="S21SNU520-11-G11"
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Plate: 11 row: G column: 11
High quality sequence stop: 646.
Location/Qualifiers
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/sex="F"
                                                                                                               BM790595.1 GI:19138827
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Fax: +82-42-860-4409
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                                                            mRNA sequence.
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RESULT 4

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/clone_lib="NIH_MGC_113"
/lab_host="DH10B (phage-resistant)"
/nab_host="DH10B (phage-resistant)"
/nat="Organ: spleen: Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; CDNA made by oligo-dT priming. Directionally cloned
into EcorI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using 2AP-CDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
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885 bp mRNA linear EST 16-JUL-2002
AGENCOURT 8351580 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6282394
5/, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                      L Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Preparation: Rubin Laboratory
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://magge.llnl.gov
Plate: LLCM2476 row: 1 column: 11
High quality Sequence stop: 599.
                                                                                                                                                                                                                                           Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Best Local Similarity 100.0%; Pred. No. 2.3e-29;
Matches 174; Conservative 0; Mismatches 0;
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/db_xref="taxon:9606"
/clone="IMAGE:6282394"
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BQ706025.1 GI:21844924
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/clone="IMAGE:3943719"
/clone="IMAGE:3943719"
/clone=Lib="NRi_MGC]"
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/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="bH10B (phage=resistant)"
/note="Crgan: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoR1; CDNA made by Oilgo-dr priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size=selected >5000p for average
insert size 1: 8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZaP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
31 a 283 c 317 g 151 t
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                   DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/ILNL at: image.llnl.gov Plate: LLCM799 row: g column: 16
High quality sequence stop: 860.
                 NIH MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
1. 992
                                                                                                  Email: cgapbs-r@mail.nih.gov
Tyssue Procurement: DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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1 (bases 1 to 992)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Unpublished (2001)
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Pred. No. 2.3e-29;
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100.0%; Pred. No. ...
0; Mismatches
                                                              Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
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AL556392
AL556392.1 GI:12899025
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Matches 174; Conservative
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                     AUTHORS
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/close_lb="LTI_NELOG_PL2"
/tissue_type="Placenta"
/tis
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Catarrhini; Hominidae; Homo.
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Unpublished (1999)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: Gapbs-rémail.nih.gov
Tissue procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov: h column: 01
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NIH-MGC http://mgc.nci.nih.gov/.
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319 c 269 g 173 t
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Pred. No. 2.3e-29;
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100.0%; Pred. No. 2..
0; Mismatches
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/tissue_type="leukocyte"
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/clone="IMAGE:5214000"
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BI907041
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cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dias Neto, E., García Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveire, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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Sta_2: Smal; A min1-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST 16-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL5&t2=IL5-EN0086-061100-237-h02&t3=2000-11-06&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 34
High quality sequence start: 34
High quality sequence stop: 171.
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IL5-EN0086-061100-237-h02 EN0086 Homo sapiens CDNA, mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 173)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          828 GAACAACAGCTCAGAACAACGIGICTCTCIGGACAIIGACCICIGGGACAAGIICAGIGA 887
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                                                                                                                                                                                                                                                     Length 700;
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000) 20202663
                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                Score 172.4; DB 13;
Pred. No. 5.1e-29;
0; Mismatches 1;
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/db_xref="taxon:9606"
/clone_lib="EN0086"
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                                                                                                                                                                                                                                                17.2%;
99.4%;
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Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                            Matches 173; Conservative
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Best Local Similarity
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 458)
M. Hilliar, L. Clark, M., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Tan, F., Trevaskis, E., Materston, R., Williamson, A.; Wohldmann, P. and Wilson, R.

The Washu-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
Mashington University School of Medicine
A444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1810
Email: est@watson.wustl.edu
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//dev_stage="adult"
//dev_stage="bill0B (ampicillin resistant)"
//dev_stage="bill0B (ampici
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profiles into the pUC 18 vector. Reverse transcription tissue mRNA and cDNA amplification were performed under low stringency conditions. " 51~c~49~g~40~t
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1583 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGCTGGGTAGAGGCCAGGCCTGTGGGGGCTGGAGCCAGGCTGAGAAGGGGTGCCATGGAG 797
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                                                                                                                                                                                                               17.0%; Score 170.4; DB 12
99.4%; Pred. No. 1.2e-28;
live 0; Mismatches 1;
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/db_xref="GDB:571655"
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High quality sequence stops: 348
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Location/Qualifiers
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R73335.1
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                     888 ACTCTCCACCAAGTGCATCATTAAGACTGTGGAGTTCGCCAAGCAGCTGCCCGGCTTCAC 947
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/lab_host="DH10B (ampicillin resistant)"
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/clone_lib="Soares breast 2NbHBst"
                                                                                                                                                                                                                            17.0%; Score 170; DB 14;
100.0%; Pred. No. 1.7e-28;
ive 0; Mismatches 0;
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/db_xref="GDB:573359"
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Seq primer: M13RP1
High quality sequence stop: 291.
Location/Qualifiers
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                                                                                                                                                                                                                                                             Best Local Similarity 100.0
Matches 170; Conservative
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(Pharmacia), digested with Not I and cloned into the Not and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot 230. Library constructed by Bento Soares and M.Fatima Bonaldo."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                    828 GAACAACAGCTCAGAACAACGTGTCTCTCTGGACATTGACCTCTGGGACAAGTTCAGTGA 887
                                                                                                                                                                                                                                                                                                              110 ACTCTCCACCAAGTGCATCATTAAGACTGTGGAGTTCGCCAAGCAGCTGCCCGGCTTCAC 169
                                                                                                                                                                                                                                                          50 GAACAACAGCTCAGAACAACGTGTCTCTGGACATTGACCTCTGGGACAAGTTCAGTGA 109
                                                                                                                                                                                                                                                                                             888 ACTCTCCACCAAGTGCATCATTAAGACTGTGGAGTTCGCCAAGCAGCTGCCCGGCTTCAC 947
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mab62b03.yl Soares_thymus_2NbMT Mus musculus cDNA clone
IMAGE:3974740 5' similar to SW:RRA_MOUSE Pil416 RETINOIC ACID
RECEPTOR ALPHA ;, mRNA sequence.
                                                                                                                                                                                    ö
                                                                                                                                                Length 367;
                                                                                                                                                                                                                                                                                                                                                                                      170 CACCCTCACCATCGCCGACCAGATCACCCTCCACAGGCTNCCTGCCTGG 219
                                                                                             4 others
                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                   948 CACCCTCACCATCGCCGACCAGATCACCCTCCTCAAGGCTGCCTGG
                                                                                                                                                Score 169; DB 14;
Pred. No. 2.7e-28;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain="CS7BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:3974740"
/clone_lib="Soares_thymus_2NbMT"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism-"Mus musculus"
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/dev_stage="4 weeks"
/lab_host="DH10B"
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High quality sequence stop: 3
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Best Local Similarity 99.4%;
Matches 169; Conservative
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AA790328 764 bp mRNA linear EST 06-FEB-1998 vw17c09.rl Soares_mammary_gland_NbMMG Mus musculus cDNA clone IMAGE:1244080 5' similar to 9b:X57528 M.musculus mRNA for retinoic acid receptor-alpha (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Rodentla; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 764)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:657768
                                                                                                      887
                                                                                                                                            147 GAACAACAGCTCAGAACAACGAGTCTCCCTGGACATTGACCTCTGGGACAAGTTCAGTGA 206
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Contact: Marra M/Mouse EST Project
WashD HHMI Mouse EST Project
WashD HHMI Mouse EST Project
WashIngton University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
     Length 424;
                                                                                                                                                                                                                                                                                                Indels
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/sex="male"
Score 167.6; DB 12;
Pred. No. 5.8e-28;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: -28m13 rev2 ET from Amersham
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/dev_stage="4 weeks"
/lab_host="DH10B"
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The WashU-HHMI Mouse EST Project
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Location/Qualiflers
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/clone="IMAGE:1244080"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA790328.1 GI:2850448
Query Match 16.7%;
Best Local Similarity 97.7%;
Matches 170; Conservative
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AA790328
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/note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6; Site_1: ECORV (destroyed); Site_2: Not1; RNA source pool of three ovaries, from females ranging in age from 38 to 49 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 2.1 kb, insert size range 1-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 036.
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NIH-WGC http://mgc.ncl.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: Invitrogen

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                              947
                                                                                                                                         222 GAACAACAGCTCAGAACAACGAGTCTCCCTGGACATTGACCTCTGGGACAAGTTCAGTGA 281
                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           366 GCAGCCTGCAGCTGCCCTCTTAACCCCCTCTGCCCTCCAGAGGAAACGACGGAA 425
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Pred. No. 1.1e-27;
0; Mismatches 23; Indels 0;
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                                                    Length 764;
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                                                                   Pred. No. 6.4e
0; Mismatches
                                                    Score 167.6;
Pred. No. 6.4
 134
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/clone="IMAGE:5587843"
/clone_lib="NIH_MGC_125"
/lab_host="DH10B"
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High quality sequence stop: 712.
Location/Qualifiers
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Plate: LLAM12357 row:
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                                                  Query Match
Best Local Similarity 97.7%;
Matches 170; Conservative
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                                                                                                                                                                                                                                                                                                         BF182871 866 bp mRNA linear EST 31-OCT-2000 601809396F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040303 5',
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 866)
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                                  485
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National Institutes of Health, Mammallan Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        366 GCAGCCTGCAGCTGCCCTCTTAACCCCCTCTGCCCTCCACAGCTGTGAGAAACGACCGAA 425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: crapbs remail.nih.gov
Tissue Procurement: DoTD/DTP/Gazdar

Tissue Procurement: DoTD/DTP/Gazdar

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can lette://image.llnl.gov

Pittp://image.llnl.gov

O column: 24

High quality sequence stop: 723.
                                GCCGACTGCAGAAGTGCTTTGAAGTGGGCATGTCCAAGGAGTCTGTGAGAAACGACCGAA
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Mismatches 23; Indels
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/lab_host="DH10B (phage-resistant)"
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/clone="IMAGE:4040303"
/clone=lib="NIH_MGC_18"
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Contact: Robert Strausberg, Ph.D.
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BE34/412 861 bp mRNA linear EST 09-AUG-2000 601072989F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3458974 5', mRNA sequence.
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I (bases 1 to 861)

S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih gov
Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Incyte Genomics, Inc.

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
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/clone="INMGE:3458974"
/clone_lib="NIH_MGC_12"
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/lab_host="DH108"
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Plate: LLAM8451 row: a column: 23
High quality sequence stop: 571.
Location/Qualifiers
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/organism="Homo saplens"
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Search completed: March 30, 2003, 13:48:26

Job time : 1300.57 secs

Mon Mar 31 17:07:59 2003

GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

March 30, 2003, 08:00:38; Search time 2122.53 Seconds (without alignments) 13725.086 Million cell updates/sec 1 gcctaaaaaattccccgtgtt........ccctccctcccactggagaa 1001 4109280 Total number of hits satisfying chosen parameters: 2054640 seqs, 14551402878 residues US-09-691-220-3_COPX_15000_16000 1001 OM nucleic - nucleic search, using sw model Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries IDENTITY_NUC Gapop 10.0 , Gapext 1.0 em_htgo_mus:* em_htgo_other:* em_htgo_hum:* em_htg_mam: * em_htg_vrt: * em_sy: * Minimum DB seq:length: 0 Maximum DB seq:length: 2000000000 em_htg_inv:*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

AX333042 Sequence X06614 Human mRNA I08117 Sequence 1 AR051122 Sequence AR052136 Sequence AR052136 Sequence AC090426 Homo sapi AC080112 Homo sapi I09348 Sequence 1	ACO13023 Homo sapinación de la Contracta de la	linear PAT 09-JAN-2002 'Vertebrata; Buteleostomi; ni; Hominidae; Homo. Ebner,R., Endress,G., tic screening using signature
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Pred. No. 6.3e-191;
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gene sets
Patent: WO 0194629-A 3551 13-DEC-2001;
Avalon Pharmaceuticals (US)
Location/Qualifiers
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TCGRQDLEQDPRVDMLQEPLLEALKVYVRKRRPSRPHMFPKNLMKITDLRSISAKGA
ERVITLKMEI PGSMPPLIQEMLENSEGLDTLSGQPGGGRDGGGLAPPPGSCSPSLSP
SSNRSSPATHSP
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DRNKKKKEVPKPECSESYTLTPEVGELIEKVRKAHQETFPALCOLGKYTTNNSSEGRV
SLDIDLWDKFSELSTKCIIKTVEFAKQLPGFTTLTIADQITLLKAACLDILILRICTR
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Giguere, V., Ong.E.S., Segul, P. and Evans, R.M.
Identification of a receptor for the morphogen retinoic acid
Nature 330 (6149), 624-629 (1987)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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/protein_id="CAA29829.1"
/db_xref="GI:36157"
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Retinoic acid receptor composition and
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Evans, R.M., Giguere, V., Ong, E.S.,
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EP 0325849.
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Dmitrovsky,E., Warrell,R.P. Jr., Miller,W.H. Jr. and Frankel,S.
Methods for detection of acute promyelocytic leukemia (APL)
Patent: US 5845642-A 3 01-DEC-1998;
Location/Qualifiers
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AR061122
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Tsai, S. and Collins, S.J.
Creating novel hematopoietic cell lines by expressing altered
retinoic acid receptors
Patent: US 5830760-A 1 03-NOV-1998;
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GTGGCTCGGAAGGGCCCCCACTCCCTTTCATGTCCCTGTGCCCCCCAGTTCTCCCC
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Sequence 1 from patent US 5830760.
AR052136 GI:5975500
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1012 c 788 g
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0; Mismatches 52;
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Submitted (14-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA. On Aug 14, 2002 this sequence version replaced g1:22123315. All repeats were identified using RepeatMasker:
                                                                         All repeats were identified with the Smit, A.P.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
Genome.center
Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                             arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            377 AGGCCTGGGCCCTCAGTGGACTGCCTGCTCCCACAGCCTGGGCTGACGTCAGAGGCCGAG
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                                                                                                                                                                                                                                                                                                                                                                           NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is
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Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@enome.wi.mit.edu
Center project Information
Center project name: L11030
Center clone name: 2267_D_19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2129 2228: gap of 100 bp 2229 157931: contig of 155703 bp in length 157932 158031: gap of 100 bp 158032 173441: contig of 15410 bp in length. Location/Qualifiers
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Submission

Barna, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 173441)

Barna, N., Bastien, V., Bloom, T., Boguslavkly, L., Boukhgalter, B., Chang, J., Chazaro, B., Chopel, Y., Collymore, A., Cooke, P., DeArellano, K., Devar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardy, B., Graham, J., Grand-Plerre, N., Hagos, B., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., McCarthy, M., Meldrim, J., Menes, L., Mihova, T., Morbu, C., Norman, C. H., Murphy, T., Naylor, J., Menes, L., Mihova, T., Morbu, C., Norman, C., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Stange, Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vossiliev, H., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., North, C., Lander, R., Wu, X., Wyman, D., Young, G., Zainoun, J., North, C., Lander, S., Wyman, D., Young, G., Zainoun, J., North, C., Lander, R., Wo, A., Willson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Roy, R., L., Zilmer, A., and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                           AC080112 173441 bp DNA linear HTG 14-AUG-2002 HOMO saplens chromosome 17 clone CTD-2267D19 map 17, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                      GTGGCTCGGAAGGGGCCCCCCACTCCTTTCATGTCCCTGTGCCCCCCAGTTCTCCTCCT
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Homo sapiens chromosome 17, clone CTD-2267D19
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Evans, R.M., Giguere, V., Ong, E.S., Segui, P.S., Umesono, K. and Thompson, C.C.
Patent: WO 8905355-A 1 15-JUN-1989;
                                                   ATACCCTGCCATACCAACCCCAGGTATTAATTCTCGCTGGTTTTGTTTTTATTTTAATTT
                                                                                 TTTTGTTTTGATTTTTTAATAAGAATTTTTCATTTTAAGCACATTTATACTGAAGGAATT
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Pred. No. 1.5e-190;
); Mismatches 53;
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Sequence 1 from Patent WO 8905355.
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Birren, B., Nusbaum, C. and Lander, E. Homo, sapiens chromosome 17, clone RP11-5809
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Homo sapiens chromosome 17 clone RP1
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Birren, B., Linton, L.,
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Pred. No. 8.1e-190;

Conservative

Similarity

Best Local

Matches

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Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehoczky, J., Levine, R., Liuck, T., Liuck, Locke, K., Macdonald, P., Marquis, N., Meckan, P., McGurk, A., McKennan, K., Meldrin, J., Meneus, L., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T.M., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vas, L., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Zimmer, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (19-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 19, 2002 this sequence version replaced g1:22123724.
All repeats were long RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Galagan, J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pleces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: sequence_submissions@genome.wi.mit.edu
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Gage, D.,
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Forrest, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="RPCI-11 Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center clone name: 58_0_9
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                                                                                                                                                                                                                                                                             Direct Submission
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                                                                                                                                                                                                                                                   and Zody, M.
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DB 2; Length 166368;

Score 868.4;

86.8%;

Query Match

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Homo sapiens chromosome 17 clone RP5-1112G21 map 17, WORKING DRAFT
SEQUENCE, 10 unordered pieces.
                                                                                                                                                                                                                                   11190 GGCCCCCCCCCCCGCCAGCTGTAGCCCCCAGCCTCAGCCCCCAGCTCCAACAGAAGCAGCCG 11249
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Homo sapiens.
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                                                                                                                                                                                            Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Baldwin, J., Barna, N., Collymore, A., Collymore, A., Collymore, K., Cooke, P., Dartellano, K., Dewarr, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardf, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Subramanian, A., Talamas, J., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vasalliev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.

Lisepats were identified and institute/MIT Center for Genome Submission

All repeats were identified using RepeatMasker:

All repeats were identified using RepeatMasker:

http://ftp.genome.washington.edu/FW/RepeatMasker.html
                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. .
1 (bases 1 to 158766)
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Center: Whitehead Institute/ MIT Center for Genome Research
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Center clone name: 1112_G 21

Sequencing vector: M13: M77815; 41% of reads
Sequencing vector: Plasmid: L08752; 43 of reads
Sequencing vector: Plasmid: L08752; 43 of reads
Sequencing vector: Plasmid: L08752; 43 of reads
Chemistry: Dye-primer-amersham: 12% of reads
Chemistry: Dye-primer-amersham: 12% of reads
Chemistry: Dye-primer phrap; version 0.96073
Consensus quality: 153948 bases at least Q40
Consensus quality: 155118 bases at least Q40
Consensus quality: 156118 bases at least Q30
Consensus quality: 157160 bases at least Q30
Insert size: 53000; agarose-fp
Insert size: 157866; s.

* NOTE: This is a "working draft' sequence. It currently
consists of 10 contigs. The true order of the pieces
is not known and their order in this sequence record is
trus of N, but the exact sizes of the gaps are unknown.
This record will be updated with the flinished sequence
as soon as it is available and the accession number will
be preserved.
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                                                                                              Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 17, clone RP5-1112G21
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ORGANISM
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D 155633 CTGTGTTCATCAAGACACCCCTCTGCCCAGCTCACCACATCTTCATCACCAGCAAAGGC 155574
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124746 156015: courts ... 100 bp
156016 156115: gap of 100 bp
156116 158766: contig of 2651 bp in length.
Location/qualifiers
                                                                                                                                                                                                                                           /clone="RP5-1112G21"
/clone_lib="RPCI Human PAC library 5"
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Best Local Similarity 99.1%; Pred. No. 1.8e-187;
Matches 863; Conservative 0; Mismatches 8;
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/note="assembly_fragment"
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                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
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Db 74627 CTGTAGCCCCAGCCTCAGCCCCAGCTCCAACAGAAGCAGCCCGGCCACCCCCCCGG 74568
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                                                                                                        Center project name: L27554

Center clone name: 1029_L16

Center clone name: 1029_L16

Sequencing vector: Plasmid: n/a: 100% of reads
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 186234 bases at least Q40
Consensus quality: 187050 bases at least Q20
Insert size: 188000; agarose-fp
Insert size: 188074; sum-of-contigs
Quality coverage: 14.6 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 188574;
                                              Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74661 74760: gap of 100 bp 74761 151113: contig of 76353 bp in length 151114: gap of 100 bp 151214 188574: contig of 37361 bp in length Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   504 others
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100.0%; Pred. No. 7.1e-186;
iive 0; Mismatches 0;
           Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vector_side:right"
. 48660 c 47029 g 43760 t
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/note="assembly_fragment"
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151214. .188574
/note="assembly_fragment
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/chromosome="17"
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2173. .19348
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Best Local Similarity 100.0
Matches 853; Conservative
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Unpublished
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Unsbeum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,
Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B.,
Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A.,
Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S.,
Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J.,
Gardyra, S., Gardam, L., Grand-Pierre, N., Hagos, B.,
Horton, L., Hulme, W., Ilievi, I., Johnson, R., Lindblad-Toh, K.,
Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C.,
McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V.,
Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C. H.,
Phunkhang, P., Plerre, N., Raymond, C., Retta, R., Rise, C., Rogov, P.,
Roman, J., Roy, A., Schauer, S., Schupback, R., Stajanovic, M., Talamas, J.,
Smith, C., Spencer, B., Stange-Thoman, N., Stojanovic, M., Talamas, J.,
Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H.,
Zembek, L., Zimmer, A. and Zody, M.,
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       188574 bp DNA linear HTG 16-AUG-2002 Homo sapiens chromosome 17 clone RP11-1029L16 map 17, WORKING DRAFT SEQUENCE, 6 unordered pleces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (16-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasKer:
Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                 DD 155453 CTGTACATACCCTGCCATACCAACCCCAGGTATTAATTCTCGCTGGTTTTGTTTTATTT 155394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db 155213 CCTCCTCAGCCTTTTCCTCCTCAGTTTTTTAAAACTGTGAAGTACTTATCAA 155154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 188574)
                                  DD 155393 TAATTITITGTTTTGATTTTTTTTAATAAGAATTTTCATTTTTAAGCACATTTATACTGAA 155334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Db 155273 GAGGGATGGCTCGGAAGGGCCCCCACTCTCCTTTCATGTCCCTGTGCCCCCCAGTTCT 155214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  910
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                                                                                                                                                                                                                                                                                             TAATTITTTTTTTTTTTTTTTTTTAAGAATTTTCATTTTAAGCACATTTATACTGAA 790
611 CAACCICCCCCTGCCTCGGTIGGIGACAGGGGGTGGGACAGGGGCGGGGGTTCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db 155333 GGAATTTGTGCTGTGTATTGGGGGGAGCTGGATCCAGAGCTGGAGGGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAGGGAGTGGCTCGGAAGGGGCCCCCACTCTCCTTTCATGTCCCTGTGCCCCCCAGTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 911 CCTCCTCAGCCTTTTCCTCCTCAGTTTTCTTTTAAAACTGTGAAGTACTAACTTTCCAA
                                                                                                                                              671 CTGTACATACCCTGCCATACCAACCCCAGGTATTAATTCTCGCTGGTTTTGTTTTTATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                               Birren B., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 17, clone RP11-1029L16
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AC131063.1 GI:22267816
HTG, HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
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REFERENCE
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1.9457	S Birren Barna, Camara	Cook, A Faro, S Gardyn	Karata Liu, G. McCart	O'Conn Phunkh Roman,	Tesfay Viel, R Zembek			Faro, s Gardyn Horton Karata	McCart Murphy O'Con	Roman, Smith, Tesfay		On Aug All re Smit,		¥0;00	Provided the provided the provided to the provided to the provided to the provided
14.05	AUTHOR					JOURNA JOURNA REFERENC	AUTHOR				TITLE JOURNA	COMMENT			
269 ACCGCCCACGCCACACACACACACACACACACACACACA		<u>.</u>													
09 26 09 26 09 26 09 32 09 32 09 32 09 36 09 36 09 56 09 56 09 56 09 7426 09 62 09 62 09 7426 09 93 09 7396 09 93 09 7396 09 93 09 7396 09 93 09 7396 09 93 09 7396 00 93 00 9	ACCGCCACGCCACATGGACACAGCCCTCGCCTCCGCCCCGGCTTTCTCTGCTTTCT	ACCGACCATGAGACCCGGACCAGCCCTGCCCCACCTGCCCTCCGGGCAGTACTGGGG 328	ACCTTCCCTGGGGGACGGGAGGAGGAGCACGACTCCTTGGACACAGGCCTGGGCCC	TCAGTGGACTGCCTCCCACAGCCTGGGCTGACGTCAGAGGCCGAGGCCAGGAACTGA 	GTGAGGCCCCTGGTCCTGGGTCTCAGGATGGGTCCTGGGGGCCTCGTGTTCATCAAGACA 508	CCCCTCTGCCCAGCTCACCACATCTTCATCACCAGCAAACGCCAGGACTTGGCTCCCCCA	TCCTCAGAACTCACAAGCCATTGCTCCCCAGCTGGGAACCTCAACCTCCCCCCTGCCTC 628	GGTTGGTGACAGAGGGGGTGGGACAGGGCGGGGGGTTCCCCCTGTACATACCTGCCAT	ACCAACCCCAGGTATTAATTCTCGCTGGTTTTGTTTTTATTTTAATTTTTGTTTTGTT 	TTTTTAATAAGAATTTTCATTTTAAGCACATTTATACTGAAGGAATTTGTGCTGTGTAT 	TGGGGGGAGCTGGATCCAGAGCTGGAGGGGTGGGTCCGGGGGAGGGA	GGGCCCCACTCTCCTTTCATGTCCCTGTGCCCCCAGTTCTCCTCTCACCTTTTCCT 928	CCTCAGTTTTCTCTTTAAAACTGTGAAGTACTAACTTTCCAAGGCCTGCCT	TCCCACTGGAGAA 1001 	AC126392 Homo sapiens SEQUENCE, 11 AC126392.2 AC126392.2 AC126392.2 HTG, HTGS_PHR human. Homo sapiens ENKaryota; Mammalis M Mammalis M Mammalis M Homo sapiens Upublished 2 (bases 1 t
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MATHORS BLITER, B. Washsam, C. Hander, E. Alli, M. 1141. N. Macherson, S. Camarata, J. Chang, J. Chazaro, S. Choped, J. Cologo, A. Coche, P. Detrellano, K., Devar, K., Diaz, J. S., Dodge, S., Coche, A., Cohe, P. Detrellano, K., Devar, K., Diaz, J. S., Dodge, S., Gardan, J. Chang, J. M. Gapo, J. Caligan, C. Caligan, S. Carban, L., Crand, Pletre, M. Hados, B. Marta, M. Gapo, J. Cand, J. Chara, M. Gapo, J. Caligan, J. Characto, B. Caligan, J. Caligan, J. Caligan, J. Characto, B. Caligan, J. Calig
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This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 30513: contig of 30513 bp in length
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                                                                                                                                                                                                                                                                                                                    66015 66114: gap of 100 bp 66115 108183: contig of 42069 bp in length 108184 108283: gap of 100 bp 108184 130510: contig of 22227 bp in length 130511 130610: gap of 100 bp 130511 166740: contig of 36130 bp in length 166741 166840: gap of 100 bp 166741 168840: gap of 100 bp 166741 190309: contig of 23469 bp in length 106841 190309: contig of 23469 bp in length.
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66014: contig of 14544 bp in length
                                                                                                                                                                                                                                           91: gap of 100 bp 51370: contig of 13579 bp in length
                                                                                                                         64: gap of 100 bp 33693: contig of 1829 bp in length
                                                                                                                                                              93: gap of 100 bp 35405: contig of 1612 bp in length
                                                                                                                                                                              33794 35405: contig of 1612 bp in length
35406 35505: gap of 100 bp
35506 37691: contig of 2186 bp in length
37792 51370: contig of 13579 bp in length
51371 51470: gap of 100 bp
                                                                                                   31764: contig of 1151 bp in length
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Pred. No. 7.9e-186;
0; Mismatches 11;
                                                                                 100 bp
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// note-"assembly_fragment"
31865. 33693
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3506. 37691
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3779. 51370
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51471. 66014
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6615. 108183
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108284. 130510
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130611. 166740
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166841. 190309
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48484 c 47543 g 45018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="RP11-1029F16"
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Best Local Similarity 98.7%;
Matches 856; Conservative
                                                                               30514 30613: 0
30614 31764
31765 31864: 0
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AC069032 187557 bp DNA linear HTG 24-AUG-2002 Homo sapiens chromosome 18 clone RPl1-185D6 map 18, WORKING DRAFT SEQUENCE, 44 unordered pieces.
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2 (bases 1 to 187557)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G.,
TICTCTGCCTTTCTACCGACCATGTGACCCCGCACCAGCCCTGCCCCCACCTGCCCTCC 314
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                                                                                                                                                                                                                                                                                      Db 130090 ACTIGGCICCCCCATCCICAGAACICACAAGCCATIGCICCCCAGCIGGGGAACCICAAC 130031
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                                                                                                                                                                                                                      130210 AGGCCAGGAACTGAGTGAGGCCCCTGGTCCTGGGTCTCAGGATGGGTCCTGGGGGCCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                          119970 ACATACCCTGCCATACCAACCCCAGGTATTAATTCTCGCTGGTTTTGTTTTATTAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db 129790 GAGTGGCTCGGAAGGGCCCCCACTCTCCTTTCATGTCCCTGTGCCCCCCAGTTCTCCTC
                                                                    AGAGGCCTGGGCCCTCAGTGGACTGCCTGCTCCCACAGCCTGGGCTGACGTCAGAGGCCG
                                                                                                                                                                                                     435 AGGCCAGGAACTGAGTGAGGCCCCTGGTCCTGGGTTCAGGATGGGTCCTGGGGGCCTCG
                                                                                                                                                                                                                                                                     TGTTCATCAAGACACCCCTCTGCCCAGCTCACCACATCTTCATCACCCAGGAAACGCCAGG
                                                                                                                                                                                                                                                                                                                                        ACTTGGCTCCCCCAFCCTCAGAACTCACAAGCCATTGCTCCCCAGCTGGGGAACCTCAAC
                                                                                                                                                                                                                                                                                                                                                                                                         675 ACATACCCTGCCATACCAACCCCAGGTATTAATTCTCGCTGGTTTTGTTTTTTTAAT
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia: Eutheria; Primates; Catarrhini; Hominidae;
I pases 1 to 187557)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 18, clone RP11-185D6
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HTG; HTGS_PHASE1; HTGS_DRAFT
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AUTHORS
 255
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Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, M., Gage, D., Galdgan, J., Cardyna, S., Ginde, S., Goyette, M., Graham, L., Grand, J., Lakocque, K., Lamazares, R., Lander, R., Ratatas, A., Klein, J., Lakocque, K., Lamazares, R., Lander, C., Ranp, L., Karatas, M., McCarthy, M., McCarth, M., McGarth, M., Morman, C., Ranp, L., Margada, C., Ranp, L., Margada, C., Manga, V., Morrow, J., Murphy, T., Maylor, J., Morman, C., H., O'Comnor, P., O'Donnell, P., O'Mall, D., Ollara, T., M., Morman, C., H., O'Comnor, P., O'Donnell, P., O'Mall, D., Ollara, T., Morman, C., Riley, R., Rogov, P., Rothman, D., Stange-Thomann, N., Schauer, S., Sepencer, S., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Taigilio, J., Vassiliev, H., Viel, R., Volan, Willson, B., Wu, X., Wyman, D., Ye, W., Viel, R., Voland, Wullson, B., Wu, X., Wyman, D., Ye, W., Viel, R., Voland, Wullson, B., Wu, X., Wyman, D., Ye, W., Santos, T., Lamer, A., and Zody, M. Collins, S., Gander, S., Charles Street, Cambridge, MA 02141, USA

Burran, M., Bastlen, V., Boybellawity, L., Boukhqalter, B., Brown, S., Gande, S., Cooke, P., DaArellano, K., Dewar, K., Diaz, J.S., Gardgan, J., Campoplano, A., Choepel, Y., Colangelo, M., Cage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Liley, L., Anderson, K., Dowar, S., Servery, P., Spencer, B., Heaford, A., Horton, L., Milne, W., Liley, L., Marthews, S., Ginde, S., Goyette, M., Graham, L., Grand Pierre, N., Matthews, C., McCarthy, M., Welley, R., Schauer, S., Schueback, M., Riley, R., Schuer, S., Schueback, S., Suugnez, C., Spencer, B., Stange-Thum, W., Yasailiev, H., Willey, R., Schuer, S., Schueback, S., Suugnez, C., Sentop, M., Yasailiev, H., Wilson, B., Wu, X., Watsailiev, M., And Zoon, W., Watsa
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Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Feb 18, 2001 this sequence version replaced gi:11225387.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome
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http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Sequencing vector: Plasmid; n/a; 98% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
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------ Project Information
Center project name: L10383
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Insert size: 183257; sum-of-contigs
Oublity coverage: 3.7 in Q20 bases; agarose-fp
Quality coverage: 3.4 in Q20 ba.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..... Summary Statistics
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                   18865: gap of 100 bp 20138: contig of 1273 bp in length 2028: gap of 100 bp 2189: contig of 161 bp in length 21979: gap of 100 bp 21877: contig of 1898 bp in length
                                                                                          of 100 bp contig of 1387 bp in length
                                                                                                                                                                 100 bp
f 1251 bp in length
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1227 bp in length
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                                                           of 1294 bp in length
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14159: contig of 1181 bp in length
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1559 bp in length
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18765: contig of 1520 bp in length
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45581: contig of 3011 bp in length
45681: gap of 100 bp
48005: contig of 2324 bp in length
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63506: contig of 4053 bp in length
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contig of 3802 bp in length
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contig of 3304 bp in length
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contig of 3942 bp in length
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contig of 4574 bp
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contig of 5698 bp
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f 1111
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12878: contig of
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5818: contig of
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17145: contig of
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42470: cont
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33191: cont
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Tsai.S. and Collins,S.J.
Creating novel hematopoietic cell lines retinnic acid receptors
Patent: US 5830760-A 3 03-NOV-1998;
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Pred. No. 3.1e-183;
0; Mismatches 0; Indels 0
                                                                                                                                      136167 136266; gap of 100 bp
136267 145578; contig of 9312 bp in length
145579 145678; gap of 100 bp
157187 157286; contig of 11508 bp in length
157187 157286; gap of 100 bp
157287 170785; contig of 13499 bp in length
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7999 bp
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/clone_lib="RPCI-11 Human
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/note="assembly_fragment"
2606. .3992
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5628. .6675
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/db_xref="taxon:9606"
/chromosome="18"
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  92490: contig of
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HSRARAIA8 1081 bp DNA linear PRI 02-NOV-1999
Homo sapiens retinoic acid receptor alpha (RARA) gene, exon 9 and
complete cds.
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Hjalt, T.A. and Murray, J.C.
Genomic structure of the human retinoic acid receptor-alphal gene 9226925
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AF088890.1:293. .441,AF088891.2:181. .322,
AF088890.1:422. .582,AF0888921.1843. .1019,
AF088893.1:326. .530,AF088894.1:156. .314,261. .1081)
/gene="RARA"
/Product="retinoic acid receptor alpha"
/AF088899.2:469. .646,AF088899.1:293. .441,
AF088891.2:181. .322,AF088892.1:422. .582,
AF088892.1:843. .1019,AF088893.1:326. .530,
AF088894.1:156. .314,261. .478)
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order(AF088888.2:1. .1450,AF088889.2:1. .1021,
AF088890.1:1. .689,AF088891.2:1. .629,AF088892.1:1.
/gene="RARA"
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Binert Submission

Submitted (01-SEP-1998) Pediatrics, University of Iowa, 140

Iowa City, IA 52242, USA
On Oct 14, 1999 this sequence version replaced gi:4160007

Location/Qualifiers.
1793 ATTTGTGTGTGTATTGGGGGGGAGCTGGATCCAGAGCTGGAGGGGTCCGGGGA
                                                                            1733 ATTTTTTTTTTTTTTTTTTTTTAATAAGAATTTTCATTTTAAGCACATTTATACTGAAGG
                                                                                                                                                                                     GGGAGTGGCTCGGAAGGGGCCCCCACTCTCCTTTCATGTCCCTGTGCCCCCAGTTCTCC
                                                                                                                                                                                                      ATTITITITGTTTTGATTTTTTAATAAGAATTTTCATTTTAAGCACATTTATACTGAAGG
                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="17"
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	Description	Genomic DNA encodi	Human cDNA differe	Lung cancer relate	Human RAR-alpha cD	DNA of clone phrar	RAR-alpha clone la	RAR-alpha gene. S	DNA encoding novel	RAR-alpha-403 domi
SUMMARIES	e e	AAL38339	ABK84517	ABL65214	AAV64991	AAN90124	AAQ81476	AAQ29338	AAS83048	AAQ81477
	DB	24	24	24	20	10	16	13	23	16
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d	Query Match	95.0	87.1	87.1	87.1	87.1	87.1	86.9	84.2	68.8
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Ü	58	52.4	5.2	840	24	ABQ35494	Oligonucleotide fo
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· O	34	51.2	5.1	10732	21	AAA10594	Gene encoding a su
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	40	49.6	. r.	320	5	AAA38185	Primer used in the
ט ט	4 4	4.04		320	517	AAA38186	
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New human nuclear hormone receptor proteins and nucleic acids, useful as models or targets for developing human therapeutic targets, and in identifying therapeutic proteins and modulators of nuclear hormone
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hormone receptor with a fully defined sequence of 457 amino acids given hormone receptor with a fully defined sequence of 457 amino acids given can the sequence of 457 amino acids given to the specification. The novel human nuclear hormone receptor peptides and nucleic acids encoding them can be used as models for the development of human therapeutic of human therapeutic targets, aid in the identification of therapeutic proteins, and serve as targets for the development of human therapeutic agents that modulate nuclear hormone receptor activity in cells and tissues that express the nuclear hormone receptor. The nucleic acids may be used as a query sequence to perform searches against sequence of atabases to identify family members or related sequences, as probes or primers, to construct recombinant vectors, to identify compounds that modulate nuclear hormone receptor nucleic acid expression, in gene therapy, and as antisense constructs to control nuclear hormone receptor gene expression in cells, tissues or organisms. The polypetides can be used to raise antibodies or to elicit an immune response, as a reagent in cassays designed to determine protein levels in biological fullads, as markers for tissues in which a corresponding protein is expressed, to identify a binding partner/ligand to develop a system for the assays and to identify compounds that modulate protein activity This polymoratide sequence represents the genomic DNA encoding the human continued in the number of not not protein of the invention.
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The invention relates to detecting (MI) granulocyte (GC) activation (GGA), by detecting the level of expression of gene(s) (GS) identified by DNA chip analysis as given in the specification, and comparing the expression level to an expression level in an unactivated
                                                                                              15600 TGGGGAACCTCAACCTCCCCCTGCCTCGGTTGGTGACAGGGGGTGGGACAGGGGCGG 15659
                                                                                                                                                                  15839
                                                                                                                                                                                                                                                                  960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and
                                         GGGTCCGGGGGAGGGGCTCGGAAGGGGCCCCCACTCTCCTTTCATGTCCCTGTGCC
                                                                                                                                                                                                                                                  CCCCAGTTCTCCTCCTCAGCCTTTTCCTCCTCAGTTTTCTCTTTAAAACTGTGAAGTACT
                                                                                                                                       TTATACTGAAGGAATTTGTGCTGTATTGGGGGGGAGCTGGATCCAGAGCTGGAGGGGGT
                           GGGGTTCCCCCTGTACATACCCTGCCATACCAACCCCAGGTATTAATTCTCGCTGGTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human cDNA differentially expressed in granulocytic cells #1088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriasis; rheumatoid arthritis; glomerulonephritis; asthma; thrombosis; cardiac reperfusion injury; renal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel disease; Crohn's disease; ulcerative colitis; periodontal disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 granulocytic cell; DNA chip; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              granulocyte activation; chronic inflammation; allergy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID No 1088; 114pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                      ABK84517 standard; cDNA; 2907
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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CC ct, where differential expression of Gs is indicative of GCA.

Also included are modulating (M2) GA by contacting GC with an agent

that alters the expression of at least one gene in Gs; (2) screening (M3)

Cf or an agent capable of modulating GCA or an inflammation (especially

chronic) in a tissue, an allergic response in a subject, exposure of a

subject to a pathogen or sterile inflammatory disease using the

CC subject to a pathogen or sterile inflammatory disease, by detecting the

chronic) in a tissue, an allergic response in a subject, exposure of a

subject to a pathogen or sterile inflammatory disease, by detecting the

chevel of expression of the gene is indicative of inflammation;

cc subject to a pathogen or sterile inflammatory disease, by detecting the

clevel of expression of the gene is indicative of inflammation;

cc the level of expression of the gene is indicative of inflammation.

cc the level of expression of the gene is indicative of inflammation.

cc (4) treating (M5) an inflammation (especially chronic) or in a tissue,

an allergic response in a subject, exposure of a subject to a pathogen

cc inflammation with an agent that modulates the expression of gene(s)

cc from GS in the tissue. M1 is useful for detecting GA; M2 is useful for

modulating GA; M3 is useful for screening an agent capable of modulating

cc GCA preferably in an inflammation in a tissue; M4 is useful for

creperfusion inflammation (especially chronic) in a tissue, an allergic

cresponse in a subject, exposure of a subject to a pathogen or sterile

inflammatory disease (e.g. psoriasis, rheumatoid arthritis,

creperfusion injury, ARDS, adult respiratory distress syndrome,

conducted disease, also bacterial infection, viral infection and M5 is

conduct repergented and agene differentially expressed in granulocytes.

CC Arthure
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94.4%; Pred. No. 3.2e-181;
tive 0; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ftp.wipo.int/pub/published_pct_sequences.
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stomach; lung; prostate; panoreas; carcinoma; antitumour; cancerous; cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
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                                                       TTTTGTTTTGATTTTTAATAAGAATTTTCATTTTAAGCACATTTTATACTGAAGGAATT
                                                                                                                                   CAGCCITITICCTCCTCAGTITICTCTTTAAAACTGTGAAGTACTAACTTTCCAAGGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                 Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
                                                                                                                                                                                                                                                                                                                                                                              Lung cancer related gene sequence SEQ ID NO:3551.
                                                                                                                                                                                                                                                             CCTTCCCCTCCCACTGGAGAA 2283
                                                                                                                                                                                                                                                     CCTTCCCCTCCCTCCACTGGAGAA 1001
                                                                                                                                                                                                                                                                                                                      ABL65214 standard; DNA; 2907 BP
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18-SEP-2000; 20000S-233617P.
20-SEP-2000; 20000S-23409P.
20-SEP-2000; 20000S-23409P.
22-SEP-2000; 20000S-23450P.
22-SEP-2000; 20000S-23450P.
25-SEP-2000; 20000S-23450P.
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25-SEP-2000, 2000US-235077P.
25-SEP-2000, 2000US-235082P.
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2000US-235134P.
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27-SEP-2000;
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The present invention describes a method (M1) for screening for an anti-neoplastic activity, determining a change in expression of at least one gene (1) of a signature gene set, where (1) expression of at least one gene (1) of a signature gene set, where (1) expression of at least one gene (1) of a signature gene set, where (1) expression is indicative of anti-neoplastic activity. (1) has cytostatic expression is indicative of anti-neoplastic activity. (1) has cytostatic activity and can be used in gene therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of MI, and the data is sufficient to convey the chemical structure and/or properties of the agent. MI can be used in the treatment of cancer such, as colon, breast, stoomach, lung, thyroid, cesophageal, ovarian, kidney, prostate or pancreatic cancer.

Infiltrating lobular cancer, squamous cell cancer, infiltrating ductal cancer, infiltrating ductal cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                            Endress G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2907 BP; 561 A; 1011 C; 789 G; 546 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 carcinoma, papillary carcinoma and Wilm's tumour.
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94.4%; Pred. No. 3.2e
ive 0; Mismatches
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                          28-SEP-2000; 200005-236028P.
28-SEP-2000; 200005-236032P.
28-SEP-2000; 200005-236033P.
28-SEP-2000; 200005-236033P.
28-SEP-2000; 200005-23613P.
29-SEP-2000; 200005-236111P.
29-SEP-2000; 200005-236111P.
29-SEP-2000; 200005-236111P.
02-OCT-2000; 200005-237173P.
02-OCT-2000; 200005-237274P.
02-OCT-2000; 200005-237294P.
02-OCT-2000; 200005-237294P.
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03-OCT-2000; 2000US-237425P
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Soppet DR,
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                        AGGCCTGGGCCCTCAGTGGACTGCCTGCTCCCACAGCCTGGGCTGACGTCAGAGGCCGAG
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                                                                                                   TTCATCAAGACACCCCTCTGCCCAGCTCACCACCATCATCACCAGCAAACGCCAGGAC
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                                                                                                                                                                                                                                                       GIGGCICGGAAGGGGCCCCCCACTCTCCTTTCATGTCCCTGIGCCCCCCAGTTCTCCTCCT
      Fusion protein; myl; retinoic acid receptor-alpha; RAR; human; acute promyelocytic leukaemia; APL; t(15;17); translocation; treatment; all-trans retinoic acid; ss.
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/product= "RAR-alpha"
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103..1491
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                                                                                                                                                                                                                                                                                                                                                   AAV64991 standard;
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This sequence encodes the human retinoic acid receptor alpha, RAR-alpha which is used in a method for identifying a subject with acute promyelocytic leukaemia (APL) resulting from a t(15;17) translocation who will respond to treatment with all-trans retinoic acid. The protein can also be used to identify a subject with indications of APL who will not respond to treatment with all-trans retinoic acid.
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 receptor-alpha"
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/note= "retinoic
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94.48;
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91US-0673838.
91US-0675084.
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Best Local Similarity 94.4
Matches 873; Conservative
                                                                                                                                                                                                Frankel
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                                                                                                                                                                                                                                      P-PSDB; AAW81964
                                                                                                                                                                     (SLOK ) SLOAN
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                                                                                  21-JUL-1993;
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                                                                                         GTGGCTCGGAAGGGGCCCCCACTCTCCTTTCATGTCCCTGTGCCCCCCAGTTCTCCTCCT
                                                                                                                                                     CAGCCTTTTCCTCCTCTTTTCTCTTTAAAACTGTGAAGTACTAACTTTCCAAGGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA of clone phRARI contg. the primary sequence of a protein (see corresp. AAP90395) that has ligand binding and transcription activating properties of retinoic acid receptor (RAR) protein. Used to make chimeric receptors,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA encoding retinoic acid receptor proteins - used to produce proteins for studying complexes with ligands and in diagnostic assays.
                                                                                                                                                                                                                                                                                                    receptor; ligand
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                                                                                                                                                                                 Location/Qualifiers
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P-PSDB; AAP90395.
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to produce receptor, to study binding complexes, for RAR-agonists and antagonists.
                                  87.1%; Score 871.8; DB 10;
94.4%; Pred. No. 3.2e-181;
11ve 0; Mismatches 52;
                     546
                     Sequence 2940 BP; 594 A; 1010 C; 790 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                 AGGCCTGGGCCCTCAGTGGACTGCCTGCTCCCACAGCCTGGGCTGACGTCAGAGGCCGAG
                                                              GCCAGGAACTGAGTGAGGCCCCTGGTCCTGGGTCTCAGGATGGGTCCTGGGGGCCTCGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                        An RAR-alpha cDNA (given in AAQ81477) was prepared that contained a truncation of sequences coding for the C-terminal 59 amino acids and part the 3' UTR of the wild-type human sequence (AAQ81476). This truncated comparated RAR-alpha-403, encodes a protein (AAR68024) containing the N-terminus, DNA-binding domain and part of the hormone-binding domain of RAR-alpha (AAR68023).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                               RAR-alpha; retinoic acid receptor alpha; hematopoietic; stem cell; differentiation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCCGCCAGGCAGCTGTAGCCCCCAGCCTCAGCCCCAGCTCCAACAGAAGCAGCCCGGCCAC
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                                                                                                                                                                                                                                                                                                                                                                     New haematopoletic stem cell lines with specific differentiation properties - made by transfected stem cells with nucleic acid encoding dominant negative suppressor of the retinoic acid receptor alpha, useful e.g. for haematopoletic reconstitution
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                             AAQ81476 standard; cDNA to mRNA; 2940
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Similarity 94.4%;
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                                                                                           RAR-alpha clone lambda-KIR
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P-PSDB; AAR68023.
                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                    28-JUL-1994;
                                                                                                                                                                                                                                                                          28-JUL-1993;
                                                                       01-SEP-1995
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                                                                                                                                                                                                                                                                                                                  Collins SJ,
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                                                  AAQ81476;
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polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as
                                                                                                                                                                                                                             2198
                                                      2018
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                                                                                                                                                  CAGCCTTTTCCTCCTCAGTTTTCTCTTTAAAACTGTGAAGTACTAACTTTCCAAGGCCTG
                       TTTTGTTTTGATTTTTAATAAGAATTTTCATTTTAAGCACATTTATACTGAAGGAATT
                                                                                                                                                                                           GIGGCICGGAAGGGGCCCCCCACTCCCTITCAIGTCCCTGTGCCCCCCCCAGITCTCCTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding novel human diagnostic protein #18852.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID No 18852; 103pp; English
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23-AUG-2000; 2000US-0649167.
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                                                                                                                                                            other neoplasias retinoic acid
                                                                         Kazizuka A, Miller WH;
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2928 BP; 582 A; 1012 C; 789 G; 545 T; 0 other;
                                                                                                                                                        for acute promyelocytic leukaemia and sing nucleic acid and encoded abnormal
                                                                                                                                                                                                             Disclosure; Page 43-46; 84pp; English.
                                                                      Frankel S,
                                          KETTERING INST CANCER.
 91US-0673838
                                                                      Evans RM,
                                                                                                                                                                                    receptor-alpha receptor
                                                                                                             WPI; 1992-349240/42.
P-PSDB; AAR27534.
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a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsable for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human hote: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pct_sequences.
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                                                                                                           Sequence 2930 BP; 565 A; 1008 C; 807 G; 550 T; 0 other;
                                                                                                                          Score 842.8; DB 23
Pred. No. 7.2e-175;
                                                                                                                                          0; Mismatches
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Similarity 93.6%;
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CDNA (AAQ81476) and insertion of stop codon
TAG at deletion site (1312-1314)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RAR-alpha; retinoic acid receptor alpha; hematopoietic; stem cell; differentiation; dominant negative; retrovirus; vector; neutrophil; monocyte; mast cell; basophil; ds.
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                                                          CCTCAGCCTTTTCCTCCTCAGTTTTCTCTTTAAAACTGTGAAGTACTAACTTTCCAAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New haematopoietic stem cell lines with specific differentiation properties - made by transfected stem cells with nucleic acid encoding dominant negative suppressor of the retinoic acid receptor alpha, useful e.g. for haematopoietic reconstitution
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100.0%; Pred. No. 3.3e-141;
1ve 0; Mismatches 0;
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                                                                                                                                                                                                          2279 CTGCCTTCCCTCCCTCGAGAA 2306
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103..1312
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Best. Local Similarity 100.
Matches 689; Conservative
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147-1500
//tag- "Human nuclear hormone receptor protein"
  CCGGGCAGTACTGGGGACCTTCCCTGGGGGACGGGAGGAGGAGGCAGCGACTCCTTGG
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And The invention relates to an isolated peptide of a novel human nuclear hormone receptor with a fully defined sequence of 457 amino acids given in the specification. The novel human nuclear hormone receptor peptides and nucleic acids encoding them can be used as models for the development of human therapeutic of human therapeutic targets, aid in the identification of therapeutic of human therapeutic agents that modulate nuclear hormone receptor activity in cells and tissues that express the nuclear hormone receptor activity in cells and tissues that express the nuclear hormone receptor. The nucleic acids may be used as a query sequence to perform searches against sequence of the used as a query sequence to perform searches against sequence of primers, to construct recombinant vectors, to identify compounds that confidentify family members or related sequences, as probes or primers, to construct recombinant vectors, to identify compounds that confidentify and as antisense constructs to control nuclear hormone receptor consector raise antibodies or to elicit an immune response, as a reagent in assays designed to determine protein levels in biological fluids, as markers for tissues in which a corresponding protein is expressed, to identify a binding partner/ligand to develop a system for the dentify compounds that modulate protein assays, and to identify compounds that modulate protein activity. This contains a seasons as a season be assays, and to identify compounds that modulate protein the human nuclear contains assays.
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                                                                                                                                                                                                           New human nuclear hormone receptor proteins and nucleic acids,
                                                                                                                           Beasley
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                                                                                                                       Di Francesco V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hormone receptor protein of the invention.
                                                                                                                       Ketchum KA,
                                                                                                                                                                                                                                                                                                Fig 1; 73pp; English.
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91.4%;
                                  11-OCT-2000; 2000US-239117P
19-OCT-2000; 2000US-0691220
05-OCT-2001; 2001WO-US31095
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Matches 656; Conservative
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P-PSDB; AAO21489.
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omosome 17; chromosome 15; PCR; primer;
                                                                                                                                                                                                                                                                                                                                        794
APL; translocation; chromosome 17; chromosome 15; PCR; primer; [t(15;17)(q21;q11-22)]; breakpoint; polymerase chain reaction; ss
                                                TTCATCAAGACACCCCTCTGCCCAGCTCACCACATCTTCATCACCAGCAAACGCCAGGAC
                                                                                                                    TIGGCICCCCCATCCTCAGAACTCACAAGCCATTGCTCCCCCAGCTGGGGGAACCTCAACCT
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67..2457
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1382..1413
/*tag= d
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976..1001
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22-MAR-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                      CCCGCCAGGCAGCTGTAGCCCCAGCTCCAGCTCCAACAGAAGCAGCCCGGCCAC 196
The sequence given shows a fusion between retinoic acid receptor (RAR) alpha and myl which is characteristic of acute promyelocytic leukemia (APL). This is caused by a translocation of a portion of the long arm of chromosome 17 onto the long arm of chromosome 15 [t(15;17)(q21;q11-22)]. The breakpoint region has been cloned and has been shown that DNA rearrangements are clustered in the region of the first intron of RAR-alpha. This sequence was isolated by polymerase chain reaction (PCR) using primers which correspond to sequences both 5′ and 3′ to the breakpoint region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2568 GCAGTACTGGGGACCTTCCCTGGGGGACGGGGAGGAGGAGGAGCAGCACCTCCTTGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2628 AGGCCTGGGCCCTCAGTGGACTGCTCCCACAGCCTGGGCTGACGTCAGAGGCCGAG
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                                                                                                                                                                                                                                                                                                                   DB 13; Length 3036;
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                                                                                                                                                                                                                                                             Sequence 3036 BP; 605 A; 1018 C; 890 G; 523 T; 0 other;
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                                                                                                                                                                                                                                                                                                                64.8%; Score 648.2; DB 13
92.5%; Pred. No. 2.9e-132;
iive 0; Mismatches 53;
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                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                           Local Similarity
mes 650; Conserv
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This sequence encodes a human myl/RAR-alpha (retinoic acid receptor alpha) fusion protein which is used in a method for identifying a subject with acute promyelocytic leukaemia (APL) resulting from a t(15;17) translocation who will respond to treatment with all-trans retinoic acid. The protein can also be used to identify a subject with indications of APL who will not respond to treatment with all-trans
2748 TICATCAAGACACCCTCTGCCCAGCTCACCACATCTTCATCACCAGGAACGCCAGGAC 2807
                                                                                                                                                                                                  2808 TIGGCICCCCCATCCTCAGAACTCACAAGCCATGCTCCCCAGCTGGGGAACCTCAACCT
                                                                                                                 ATACCCTGCCATACCAACCCCAGGTATTAATTCTCGCTGGTTTTGTTTTTATTTTAATTT
                                                   TTGGCTCCCCCATCCTCAGAACTCACAAGCCATTGCTCCCCAGCTGGGGAACCTCAACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Diagnosis of acute promyelocytic leukaemia - by detecting nucleic acid encoding abnormal retinoic acid receptor-alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fusion protein; myl; retinoic acid receptor-alpha; RAR; humai acute promyelocytic leukaemia; APL; t(15;17); translocation; treatment; all-trans retinoic acid; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
67..3460
/*tag= a
/*product= "myl/RAR-alpha fusion protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3036 BP; 605 A; 1018 C; 890 G; 523 T; 0 other;
                                                                                                                                                                                                                                                 Frankel S, Miller WH, Warrell RP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SLOK ) SLOAN KETTERING INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 4A-G; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human myl/RAR-alpha fusion protein
                                                                                                                                                                                                                                                                                                                                                                      ВР
                                                                                                                                                                                                                                                                                                                                                                    AAV64990 standard; cDNA; 3036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93US-0095728.
91US-0673838.
91US-0675084.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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P-PSDB; AAW81963.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 retinoic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1993;
22-MAR-1991;
22-MAR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes a composition which comprises two antisense oligonucleotides. The first oligonucleotide is specific for a cytoplasmic oncogene or proto-oncogene selected from ras, raf, EGF-1, c-fms, c-ros, c-kit, c-met, c-trk, c-src, c-abl, bcr-abl, c-fgr and c-yes. The second oligonucleotide is specific for a nuclear oncogene or proto-oncogene selected from myc, jun, c-ets, c-fos, c-myb, B-myb, c-rel, c-vav, c-ski, c-spi, cyclin Dl, PML/RAR alpha, AMLL/MTG8, c-rel, c-vav, c-ski, c-spi, cyclin Dl, p-mucleotides and such and all-l/AR-1. AR-1 and ALL-l/AR-1 for composition is used for treating cancer. The composition of antisense oligonucleotides has synergistically enhanced ability to inhibit growth of cancer cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents an oncogene from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2447
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                                                                                                                                                                                                                                                                                                                                                     itcancer composition comprising two anti-sense oligo:nucleotide(s) targetting cytoplasmic and nuclear oncogene(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2688 GCCAGGAACTGAGTGAGGCCCCTGGTCCTGGGTCTCAGGATGGGTCCTGGGGGCCTCGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTCTGCCTTTCTACCGACCATGTGACCCCGCACCAGCCCTGCCCCCACCTGCCCTCCCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCCAGGAACTGAGTGAGGCCCCTGGTCCTGGGTCTCAGGATGGGTCCTGGGGGCCTCGTG
                                    Human; oncogene; proto-oncogene; neoplastic disease; anticancer; cancer; antisense oligonucleotide; PML/RARalpha; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64.8%; Score 648.2; DB 19; Length 3036; 92.5%; Pred. No. 2.9e-132; Live 0; Mismatches 53; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3036 BP; 605 A; 1018 C; 890 G; 523 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                         1; Column 145-150; 92pp; English.
                                                                                                                                                                                                                                                        JEFFERSON THOMAS
      PML/RARalpha oncogene
                                                                                                                                                                                                                       94US-0306691
                                                                                                                                                                                      94US-0306691
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                                                                                                                                                                                                                                                                                       Calabretta B, Skorski
                                                                                                                                                                                                                                                                                                                        WPI; 1998-229882/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                        (UYJE-) UNIV
                                                                                                                                                                                    15-SEP-1994;
                                                                                       Homo saplens
                                                                                                                                                                                                                       15-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Simines 650;
                                                                                                                     US5734039-A.
                                                                                                                                                     31-MAR-1998
                                                                                                                                                                                                                                                                                                                                                        Anticancer
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        Human
                                                                                                                                                                                                                                                                                                                                                                                                         Claim
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Matches
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                      Gaps
                                        2388 CCGCCAGGCAGCTGTAGCCCCAGCCTCAGCCCCAGCTCCAACAGAAGCAGCCCGGCCAC
                                                                                                                                      2448 CCACTCCCCGTGACCGCCCACGCCCACGCCACGCCCTCGCCCTCGCCCCCCGGCTTTT
                                                                                                                                                                             2748 TICATCAAGACACCCCTCTGCCCAGCTCACCACATCTTCATCACCAGCAAACGCCAGGAC
                                                                                                                                                                                                                                                                                                                                                                                    CCCGCCAGGCAGCTGTAGCCCCCAGCCTCAGCCCCCAGCTCCAACAGAAGCAGCCCGGCCAC
                                                                                                                                                                  CTCTGCCTTTCTACCGACCATGTGACCCCGGCACCAGCCCTGCCCCACCTGCCCTCCCGG
                                                                                                                                                                                                           GCAGTACTGGGGACCTTCCCTGGGGGACGGGAGGAGGAGGCAGCGACTCCTTGGACAG
                                                                                                                                                                                                                     AGGCCTGGGCCCTCAGTGGACTGCCTGCTCCCACAGCCTGGGCTGACGTCAGAGGCCGAG
                                                                                                                                                                                                                                                                                                                                   TTCATCAAGACACCCCTCTGCCCAGCTCACCACATCTTCATCACCAGCAAACGCCAGGAC
                                                                                                                                                                                                                                                                                                                                                                          TTGGCTCCCCCATCCTCAGAACTCACAAGCCATTGCTCCCCAGCTGGGGAACCTCAACCT
                                                                                                                                                                                                                                                                                                                                                                                                                   CCCCCTGCCTCGGTTGGTGACAGAGGGGGTGGGACAGGGGCGGGGGGGTTCCCCCTGTAC
                                                                                                                          CCACTCCCCGTGACCGCCCACGCCACATGGACACAGCCCTCGCCCTCCGCCCCGGCTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATACCCTGCCATACCAACCCCAGGTATTAATTCTCGCTGGTTTTGTTTTTTTAATTT
Length 3036;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       External guide sequence; EGS; RNAse P; human; ribozyme; catalytic RNA; antiviral, hepatitis B virus; HBV; anticancer; acute promyelocytic leukaemia; retinoic acid receptor-alpha; RAR-alpha; PML; fusion gene; ss.
                     53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTTTGTTTTGATTTTTTAATAAGAATTTTCATTTTAAGCACA 779
 Score 648.2; DB 20
Pred. No. 2.9e-132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human PML/alpha-RAR fusion gene, SEQ ID NO:13.
                    0; Mismatches
64.8%;
92.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-SEP-2000 (first entry)
                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAA38656 standard;
           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US6057153-A.
                    Matches 650;
  Query Match
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           Local
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Thoomic teoprotein RMSA P, which is involved in the processing of trans. Thomic teoprotein RMSA P, which is complementary to the target RNA sequence. The sequence which is complementary to the target RNA sequence. The creognition arm which is complementary to the target RNA sequence. The creognition arm which is corpus acceptor stem and the D stem of trans. The A recognition arm is located at the 3' end of the EGS and the D at the 5' correspond to the aminoacyl sequence forms a structure corresponding to the T stem and T loop of precursor tRNA. The modified EGSs of the chargeting sequence transponding to the T stem and T loop of precursor tRNA. The modified EGSs of the coording the A and D arms, and the T stem and loop can consist of the molatied. The A and D arms, and the T stem and loop can consist of ribonucleotides with 5' phosphorothioate linkages;

C' "modified Thomic Leotides With 5' phosphorothioate linkages;

C' "modif
                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to modified human RNAse P external guide sequences (BGSs). The BGS is a ribozyme which forms the catalytic domain of the ribonucleoprotein RNAse P, which is involved in the processing of tRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2922
                                                                                                                                                                                                                                                                                                             cleaving hepatitis viral RNA comprises RNAse P targeting sequence and recognition sequence complementary to targeted sequence in target RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     317 GCAGTACTGGGGACCTTCCCTGGGGACGGGAGGAGGAGGCAGCGACCTCCTTGGACAG 376
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                                                                                                                                                                                                                                                                                      eukaryotic RNAse P for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCCGCCAGGCAGCTGTAGCCCCCAGCTCAGCCCCCAGCTCCAACAGAAGCAGCCCGGCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTCTGCCTTTCTACCGACCATGTGACCCCGCACCAGCCCTGCCCCACCTGCCCTCCCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 648.2; DB 21;
Pred. No. 3.1e-132;
0; Mismatches 53;
                                                                                                                                                                                                  George ST,
                                                                                                                                                                                                                                                                                        modified external guide sequences for
                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Column 45-48; 76pp; English.
                                                                                                                                                                                                  Werner M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64.8%;
92.5%;
                                           97US-0892747
                                                                                    95US-0372556
96WO-US00513
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Matches 650; Conservative
                                                                                                                                                                                                  Goldberg AR,
                                                                                                                                                                                                                                             WPI; 2000-399010/34.
                                                                                                                                                    (UYYA ) UNIV YALE.
                                                                               13-JAN-1995;
19-JAN-1996;
                                         14-JUL-1997;
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TTCATCAAGACACCCCTCTGCCCAGCTCACCACATCTTCATCACCAGCAAACGCCAGGAC
                                                                                                                                                                                     ATACCCTGCCATACCAACCCCAGGTATTAATTCTCGCTGGTTTTGTTTTTTTAATTT
                       AGGCCTGGGCCCTCAGTGGACTGCCTGCTCCCACAGCCTGGGCTGACGTCAGAGGCCGAG
                                                       GCCAGGAACTGAGGCCCCCTGGTCCTGGGTCTCAGGATGGGTCCTGGGGGCCTCGTG
                                                                                                                       TTGGCTCCCCCATCCTCAGAACTCACAAGCCATTGCTCCCCCAGCTGGGGAACCTCAACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                      / cas "base n at position 1477 is not identified in the specification" 1725..3511
                                                                                                                                                                                                                                                                                                                                         Hammerhead ribozyme; acute promyelocytic leukaemia; APL;
lymphoma; therapy; PML-RAR-alpha; retinoic acid receptor;
external guide sequence; EGS; antisense; ss.
                                                                                                                                                                                                                            TITIGITITICATITITIAATAAGAATTITCATITITAAGCACA 779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "RAR-alpha DNA
                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                                                            ВР
                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= a
/note= "PML DNA"
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                                                                                                                                                                                                                                                                            standard; cDNA; 3511
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                                                                                                                                                                                                                                                                                                                          PML-RAR-alpha DNA sequence.
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                                                                                      PML-RAR-alpha DNA (AAT33259) is associated with acute promyelocytic leukaemia (APL). APL is characterised by a balanced, reciprocal translocation between the long arms of chromosomes 15 and 17, resulting in a fusion of the retinoic acid receptor gene (RAR-alpha) and a gene for a putative transcription factor, PML. Methods for treating APL involve the use of ribozymes, external guide sequences and antisense oligonucleotides (see also AAT33245 and AAT33245) the specifically cleave the PML-RAR-alpha fusion mRNA (see also AAT33251) but not wild-type RAR-alpha mRNA. Plasmids carrying portions of the PML-RAR-alpha and RAR-alpha genes (see also AAT33260) allow synthesis of shortened versions of APL mRNA in vitro, facilitating testing and screening processes.
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           RNA construct(s) including ribozyme(s) and antisense oligo:nucleotide(s) - for the inactivation of RNA a: e.g. promyelocytic leukaemia or follicular lymphoma
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                                                                                                                                                                                                                                                                                                    Score 645; DB 17;
Pred. No. 1.5e-131;
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                                                                 Example 1; Page 50-52; 81pp; English
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Matches 648; Conservative
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Search completed: March 30, 2003, 10:14:57 Job time : 250.299 secs

Appli

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GENERAL INFORMATION:
APPLICANT: WARRELL JR, RAYMOND P
APPLICANT: WARRELL, JR, RAYMOND P
APPLICANT: MILLER JR, WILLSON H
APPLICANT: FRANKEL, STANLEY
TITLE OF INVENTION: METHODS FOR THE DETECTION AND
TITLE OF INVENTION: TREATMENT OF ACUTE PROMYELOCYTIC LEUKEMIA (APL)
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
   Sequence 1, M. Sequence 2, M. Sequence 1, M. Sequence 1, M. Sequence 1, M. Sequence 1, M. Sequence 13, M. Sequence 5, M. Sequence 1, M. Sequence 2, M. Sequence 1, M. Sequence 22, M. Sequence 1, M. Sequence 22, M. Sequence 1, M. Sequence 22, M. Sequen
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Sequence
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US-09-245-281-1
US-09-470-271-2
US-09-470-3598-1
US-08-487-8268-13
US-08-473-9818-5
US-08-473-9818-5
US-08-474-087-5
US-08-474-087-5
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US-08-450-272-22
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SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/095,728B
FILING DATE: 21-JUL-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/673,838
FILING DATE: 22-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WHITE, JOHN P
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 38694-A
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 2928 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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STREET: 1185 AVENUE OF THE AMERICAS
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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IMMEDIATE SOURCE:
CLONE: hRAR ALPHA
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CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10036
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MOLECULE TYPE:
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LOCATION:
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Sequence 1, Appli
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Sequence 11, Appli
Sequence 12, Appli
Sequence 14, Appli
Sequence 16, Appli
Sequence 16, Appli
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'2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
                           GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-892-747-13

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US-09-165-264-13

US-09-165-264-14

US-09-191-17-17
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US-09-243-560B-1
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3.3e-208;
                                                Mismatches
                            11arity 94.4%; Score 871.8; Starity 94.4%; Pred. No. 3.3 Conservative 0; Mismatches
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; OTHER INFORMATION:
US-08-095-728B-3
                                    Similarity
                                             873;
                            Query Match
                                      Local
                                             Matches
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                                APPLICANT: Sloan-Kettering Institute, For Cancer Research
TITLE OF INVENTION: METHODS FOR DETECTION AND TREATMENT OF
NUMBER OF SEQUENCES:
CORRESPONDENCE S:
ADDRESSE: COOPER & DUNHAM
STREET: 30 ROCKEFELLER PLAZA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 871.8; DB 5;
Pred. No. 3.3e-208;
0; Mismatches 52;
                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/02320A
Sequence 3, Application PC/TUS9202320A
GENERAL INFORMATION:
APPLICANT: Sloan-Kettering Institut
                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 22-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION TOWNER: US 673,838
FILING DATE: 22-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WHITE, JOHN PREGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                 : PC-DOS/MS-DOS
                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 38
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (212) 977-9550
(212) 644-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87.18;
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Best Local Similarity 94.4
Matches 873; Conservative
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CT-US92-02320A-3
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STRANDEDNESS:
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                                                                                                                                                         STATE: NE COUNTRY:
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                       NAME: Broderick, Thomas F.
REGISTRATION NUMBER: 31,332
REFERENCE/DOCKET NUMBER: FHCR-1-7190
TELECOMMULIATION INFORMATION:
TELEPHONE: 1-206-682-8100; 1-206-224-0709(direct)
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                      ; DB 2;
.3e-208;
                                                                                                                                                                                                                                                                    Pred. No. 3.36
; Mismatches
                                                                                                                                                                                                                                                      87.1%; Score 871.8;
94.4%; Pred. No. 3.30
                                                                                                                                                                      MOLECULE TYPE: CDNA to mRNA
DESCRIPTION: see Figure 16B; RAR-alpha
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FILING DATE: July 28, 19 ATTORNEY/AGENT INFORMATION:
                                                                                                                     LENGTH: 2940 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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hes 873; Conserv
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LIBRARY: CDNA
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                            AGGCCTGGGCCCTCAGTGGACTGCCTGCTCCCACAGCCTGGGCTGACGTCAGAGGCCGAG
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                                                                                                                                  TTCATCAAGACACCCCTCTGCCCAGCTCACCACATCTTCATCACCCAGCAAACGCCAGGAC
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TITLE OF INVENTION: "Hematopoletic Cell Lines
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Call: 5-2-2
CAMPUTER READABLE FORM:
MEDIUM TYPE: Diskette-5.25 inch, 1.2Mb
CAMPUTER: IBM PC/386 COMPatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Word for Windows 5.01-t
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,383
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/099,242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08592383
Patent No. 5830760
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APPLICANT: TSA1,
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CITY: Seattle
STATE: Washingt
COUNTRY: USA
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US-08-592-383-1
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08/099,242
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/099,24
FILING DATE: July 28, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Broderick, Thomas F.
REFERENCE/DOCKET NUMBER: 31.332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MS-DOS 4.
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TELEPHONE: 1-206-682-8100;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DESCRIPTION: particular description of the particular description 
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STATE: Washing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-592-383-3
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917 CAGCCTTTTCCTCCTCAGTTTTCTCTTTAAAACTGTGAAGTACTAACTTTCCAAGGCCTG
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                                                 857 GTGGCTCGGAAGGGGCCCCCACTCTCCTTTCATGTCCCTGTGCCCCCCAGTTCTCCTCCT
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PREDICATE: FVANS. RONALD M.; ONG, ESTELITA S.; SEGUI,
PRUDIARA S.; THOMPSON, CATHERINE C.; UEMSONO, KAZUHIKO
GUGUERE, VINCENT
TITLE OF INVENTION: RETINOIC ACID RECEPTOR COMPOSITION
WINDER OF SEQUENCES: 2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/546,256
FILING DATE: 06-0403-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 276,536
FILING DATE: 30-0403-1988
APPLICATION NUMBER: 128,331
FILING DATE: 02-DEC-1987
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Pred. No. 3.3e-208
0; Mismatches 52
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94.4%;
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Best Local Similarity 94.4
Matches 873; Conservative
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APPLICANT: TSAI, S. and S.J. Collins
TITLE OF INVENTION: "Hematopoletic Cell Lines Bearing Altered Retinoic Acid
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
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                                                              TTTTGTTTTGATTTTTTAATAAGAATTTTCATTTTAAGCACATTTATACTGAAGGAATT
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MEDIUM TYPE: Diskette-5.25 inch, 1.2Mb storage COMPUTER: IBM PC/386 Compatible
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APPLICATION NUMBER: US/08/592,383
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCTTCCCTCCCTCCCACTGGAGAA 1001
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; TOPOLOGY:
US-08-306-691B-52
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Matches
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Patent No. 5734039
GENERAL INFORMATION
APPLICANT: Calabretta, Bruno
APPLICANT: Skorski, Tomasz
TITLE OF INVENTION: ANTISENSE
TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
NUMBER OF SEQUENCES: 55
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                                      Gaps
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                                                                                                                                                  CGTGTTCATCAAGACGCCCTCTGCCCAGCTCACCACATCTTCATCACCAGCAAACGCCA
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                       Length 2658;
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                     68.8%; Score 689; DB 2; Le
100.0%; Pred. No. 1.3e-162;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                       CCTGCCTTCCCTCCTCCACTGGAGAA 1001
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                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 19102
                             Similarity
                      Query Match |
Best Local Simi
Matches 689;
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US-08-306-691B-52
 ; LIBRARY:
US-08-592-383-3
LIBRARY:
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2388 CCCGCCAGGCAGCTGTAGCCCCAGCCTCAGCCCCAGCTCCAACAGAAGCAGCCCGGCCAG
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92.5%; Pred. No. 2.1e-152;
tive 0; Mismatches 53;
                       ð
                       720
                                           SOFTWARE: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/306,691B
FILING DATE: September 15, 1994
CLASSIFICATION: 514
COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.50 inch,
                                                                                                                                                                                                                                                                     NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 8321-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-539
TELEX: No. 5734039e
INFORMATION FOR SEQ ID NO: 52:
                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 3036 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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es 650; Conserv
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2688 GCCAGGAACTGAGTGAGGCCCCTGGTCCTGGGTCTCAGGATGGGTCCTGGGGGCCTCGTG 2747
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TITLE OF INVENTION: METHODS FOR DETECTION AND TREATMENT OF CANCER
NUMBER OF SEQUENCES: 6
CORRESPONDERS: ADDRESS:
ADDRESSEB: COOPER & DUNHAM
STREET: 30 ROCKEFELLER PLAZA
                                               2448 CACTCCCGTGACCGCCACGCCACACACACCCTCGCCCTCCGCCCCGGCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       497 ITCATCAAGACACCCCTCTGCCCAGCTCACCACTCTTCATCACCAGCAAACGCCAGGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application PC/TUS9202320A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 675,084
FILING DATE: 22-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 673,838
FILING DATE: 22-MAR-1991
ATTONNEY/AGENT INFORMATION:
NAME: WHITE, JOHN P
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-noconcurrent of the companion of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 10112
COMPUTER READABLE FORM:
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U
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APPLICANT: DMITROVSKY, ETHAN
APPLICANT: WARRELL JR, RAYHOND P
APPLICANT: MILLER JR, WILSON H
APPLICANT: FRANKEL, STANLEY
TITLE OF INVENTION: METHODS FOR THE DETECTION AND
TITLE OF INVENTION: TREATMENT OF ACUTE PROMYELOCYTIC LEUKEMIA (APL)
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                              TITIGITITGATITITIAATAAGAATTITCATITIAAGCACA 779
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Pred. No. 2.1e-152;
0; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.24
CURREWT APPLICATION DATA:
APPLICATION NUMBER: US/08/095,728B
FILING DATE: 21-JUL-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/673,838
FILING DATE: 22-MAR-1991
ATTONEY,AGENT INFORMATION:
NAME: WHITE, JOHN P
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 38694-A
TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEPHONE: (212) 278-0400
TELEPHONE: (212) 391-0525
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: COOPER & DUNHAM LLP
STREET: 1185 AVENUE OF THE AMERICAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08095728B Patent No. 5843643 GENERAL INFORMATION:
APPLICANT: DMITROVSKY, ETHAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64.8%;
92.5%;
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 92.5
Matches 650; Conservative
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COMPUTER READABLE FORM:
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LOCATION: 67.2457
OTHER INFORMATION:
US-08-095-728B;1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
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STATE: NEW YORK
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMMEDIATE SOURCE:
CLONE: MYL-RAR
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2863 CCGCCAGGCAGCTGTAGCCCCAGCCTCAGCCCCAACAGAAGCAGCCCGGCCAC 2922
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 3511;
                                                            GENERAL INFORMATION:
APPLICANT: Shaji T. George, Michael Ma, Martina Werner,
APPLICANT: Shaji T. George, Michael Ma, Martina Werner,
APPLICANT: Umberto Pace and Allan R. Goldberg
TILLE OF INVENTION: Stabilized External Guide Sequences
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KET: misc_feature

LOCATION: 1..3511

COTHER INFORMATION: /function= "PML-RAR' DNA Sequence.
                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURREPY APPLICATION DATA:
APPLICATION NUMBER: US/08/892,747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64.8%; Score 648.2; DB 3;
llarity 92.5%; Pred. No. 2.2e-152;
Conservative 0; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/372,556
FILING DATE: January 13, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/00513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: January 19, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PADST, PATREA L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: ILI109C
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECAX: (404) 873-8794
TELECAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 3511 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single
                                  Sequence 13, Application US/08892747 Patent No. 6057153
                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: CDNA
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Matches 650; Conserv
                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 30309-3450
                                                                                                                                                                                                                                       Georgia
                                                                                                                                                                                                                  CITY: Atlanta
STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL:
 RESULT 9
US-08-892-747-13
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                                                                                                                                                                                                                                                                                                                                    ; DB 5;
                                                                                                                                                                                                                                                                                                                                   64.8%; Score 648.2;
92.5%; Pred. No. 2.1e
ive 0; Mismatches
                             TELEPHONE: (212) 977-9550
TELEFAX: (212) 644-0525
TELEX: (212) 42523 COOP UI
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3036 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
REFERENCE/DOCKET NUMBER: 38
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 92.5
Matches 650; Conservative
                                                                                                                                                                                                                                                 CDS
67..2457
                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: CDNA
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                 LOCATION: 67..245;
COTHER INFORMATION:
PCT-US92-023208-1
                                                                                                                                                                                                                  CLONE: MYL-RAR
                                                                                                                                                                                                                                                   NAME/KEY:
                                                                                                                                                                                                                                                                                                                                      Query Match
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CTCTGCCTTTCTACCGACCATGTGACCCCGCACCAGCCCTGCCCCACCTGCCCTCCCGG 316

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MOLECULE TYPE: CDNA to mRNA DESCRIPTION: page 11, RAR-alpha N-terminal region; positions 1396 to 1488
                                                                                                                                                                                                                                                                                                                               131 GGCCCCCCCCCCAGGCAGCTGTAGCCCCAGCCTCAGCCCCAGCTCCAACAGAAGCAGCCC 190
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                                                                                                                                                                                                                                                                                                                                                           18 GGCCCCCCCCCCCGCCAGGCAGCTGTAGCCCCCAGCCCCAGCTCCAACAGAAGCAGCCC
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                                                                                                                                                                                                                 DB 2; Le
2.5e-10;
hes 0;
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42.8%; Pred. No. 0.00034;
tive 0; Mismatches 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 11, Application US/09165264
Patent No. 6197510
GENERAL INFORMATION
APPLICATION:
TITLE OF INVENTION: Multi-Loci Genomic Analysis
FILE REFERENCE: 44747
CURRENT FILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 14
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Patent No. 6197510
GENERAL INFORMATION:
APPLICANT: Viayagamoorthy, Thuratayah
TITLE OF INVENTION: Multi-Loci Genomic Analysis
                                                                                                                                                                                                                 7.6%; Score 76; DB 100.0%; Pred. No. 2.5
Live 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                            191 GGCCACCCACTCCCCG 206
                                                                                                                                                                                                                                                                           76; Conservative
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Matches 113; Conservative
double
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                            linear
                                                                                DESCRIPTION: p
IMMEDIATE SOURCE:
                                                                                                                                       CDNA
STRANDEDNESS:
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US-09-165-264-11/c
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US-09-165-264-8/c
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SEQ ID NO 11
LENGTH: 320
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US-08-592-383-8
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Patent No. 5830760
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Tsai, S. and S.J. Collins
APPLICANT: Total
APPLICANT: Team
APP
                                                                                                                                       3102
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                                                                                                                                                                                                                                                                                                                                 3223 TTCATCAAGACACCCCTCTGCCCAGGTCACCACATCTTCATCACCAGCAAACGCCAGGAC 3282
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                         CTCTGCCTTTCTACCGACCATGTGACCCCGCACCAGCCCTGCCCCCACCTGCCCTCCCGG
                                                                                                          3103 AGGCCTGGGCCCTCAGTGGACTGCCTGCTCCCACAGCCTGGGCTGACGTCAGAGGCCGAG
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                                                                                   AGGCCTGGGCCCTCAGTGGACTGCCTCCCACAGCCTGGGCTGACGTCAGAGGCCGAG
                                                                                                                                                                                                                                                                                                          GCCAGGAACTGAGTGAGGCCCCTGGTCCTGGGTCTCAGGATGGGTCCTGGGGGCCTTCGTG
                                                                                                                                                                                                                                                                                                                                                                                                                     TTCATCAAGACACCCCTCTGCCCAGCTCACCACATCTTCATCACCCAGCAAACGCCAGGAC
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                                                                                                                                                                                                                    ADDRESSEE: Christensen, O'Connor, Johnson and Kindness STREET: 2800 Pacific First Centre, 1420 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTTTGTTTTGATTTTTAATAAGAATTTTCATTTTAAGCACA 779
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette-5.25 inch, 1.2mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Broderick, Thomas F.
REGISTRATION NUMBER: 31,332
REFERENCE/DOCKET NUMBER: FHCR-1-7190
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: MS-DOS 4.01
SOFTWARE: Word for Windows 5.01-t
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SYSTEM: MS-DOS 4.01
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/099,242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
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nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Seattle
STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98101
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                         2983
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                                           ; OTHER INFORMATION: Description of Artificial Sequence:Primer sequence US-09-165-264-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE: OTHER INFORMATION: Description of Artificial Sequence:Primer sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            182 AAGCAGCCGGCCACCCACTCCCCGTGACCGCCCACGCCACATGGACACAGCCCTCGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
4.9%; Score 49.4; DB 4; Length 320;
Best Local Similarity 42.3%; Pred. No..0.0019;
Matches 107; Conservative 0; Mismatches 146; Indels
                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Vinayagamoorthy, Thuraiayah
TITLE OF INVENTION: Multi-Loci Genomic Analysis
FILE REFERENCE: 44747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 14, Application US/09165264
Patent No. 6197510
GENERAL INFORMATION:
APPLICANT: Vinayagamoorthy, Thuralayah
TITLE OF INVENTION: Multi-Loci Genomic Analysis
FILE REFERENCE: 44747
CURRENT FILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/165,264
CURRENT FILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 7
LENGTH: 320
                                                                                                                                                                                                  Sequence 7, Application US/09165264 Patent No. 6197510
                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial Sequence
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US-09-165-264-14/c
                                                                                                                                                                  RESULT 14
US-09-165-264-7/C
                                                                                       313 CC 314
                                                                                                           CC 72
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                                                                                                                                                                                                              Length 319;
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42.6%; Pred. No. 0.0017;
tive 0; Mismatches 139; Indels
                                                                                                                                                                                                         Score 50.2; DB 4; Length 3
Pred. No. 0.0012;
0; Mismatches 143; Indels
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GENERAL INCOMMATION:
APPLICANT: Vinayagamoorthy, Thuraiayah
TITLE OF INVENTION: Walti-Loci Genomic Analysis
FILE REPERENCE: 44747
CURRENT APPLICATION NUMBER: US/09/165,264
CURRENT FILING DATE: 1998-10-01
NUMBER OF SEQ'ID NOS: 14
SEQ ID NO 13
LENGTH: 320
LENGTH: 320
TYPE: DNA
ORGANISM: Artificial Sequence
FILE REFERENCE: 44747
CURRENT APPLICATION NUMBER: US/09/165,264
CURRENT FILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 8
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Patent No. 6197510
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Best Local Similarity 42.6%;
Matches 106; Conservative 0
                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 42.68
Matches 103; Conservative
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                                     0; Gaps
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Search completed: March 30, 2003, 13:57:00 Job time: 59.7584 secs

Sequence 12, Appl Sequence 12, Appl Sequence 29, Appl Sequence 529, Appl Sequence 3950, Appl Sequence 3871, Appl Sequence 219, Appl Sequence 211, Appl

US-09-764-846-136 US-09-974-300-836

ALIGNMENTS

Sequence 4582, Apple Sequence 361, Apple Sequence 19, Apple Sequence 13, Apple Sequence 37, Apple Sequence 3, Apple Sequence 7233, Apple Sequence 7233, Apple Sequence 359, Apple Sequence 18, Apple Sequen

US-09-960-352-4582 US-09-910-943-361 US-09-764-870-40 US-09-764-903-19 US-09-925-301-351

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Sequence 524, Application US/09954456

Patent No. US20020115057a1

GENERAL INFORMATION:
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Usin Filter Persons Filter Process for Identifying Anti-Cancer Therapeutic Agents Usin Filter Persons Filter Process for Identifying Anti-Cancer Therapeutic Agents Usin Filter Persons Sets
FILE REFERENCE: 689290-76
CURRENT APPLICATION NUMBER: US/60/233,617
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US/60/234,052
PRIOR APPLICATION NUMBER: US/60/234,052
PRIOR PILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
PRIOR PILING DATE: 2000-09-26
PRIOR PILING DATE: 2000-09-26
PRIOR PILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,637
PRIOR APPLICATION NUMBER: US/60/235,711
PRIOR APPLICATION NUMBER: US/60/235,720
PRIOR APPLICATION NUMBER: US/60/235,720
PRIOR APPLICATION NUMBER: US/60/235,720
PRIOR APPLICATION NUMBER: US/60/235,720
PRIOR PRIOR APPLICATION NUMBER: US/60/235,840
PRIOR PILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,863
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,863
                                                                                                                                                             0.509-904-968A-1

0.05-09-904-568A-1

0.05-09-96-352-3453

0.05-09-96-352-3453

0.05-09-96-352-31-359

0.05-09-925-301-359

0.05-09-925-415-18

0.05-09-925-45-529

0.05-09-954-456-529

0.05-09-960-352-3371

0.05-09-960-352-3371

0.05-09-960-352-3155

0.05-09-960-352-3155

0.05-09-960-352-3159

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Best Local Similarity 94.4%;
Matches 873; Conservative
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; ORGANISM: Homo sapiens
US-09-954-456-524
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Sequence 47, Appl
Sequence 16, Appl
Sequence 18, Appl
Sequence 29, Appl
Sequence 29, Appl
Sequence 182, Appl
Sequence 1454, A
Sequence 11784, A
Sequence 392, Appl
Sequence 11784, A
Sequence 392, Appl
Sequence 11, Appl
Sequence 11, Appl
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11242.392 Million cell updates/sec
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Sequence 614, App
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                                                                                                                                                                                                                      Title: US-09-691-220-3_COPY_15000_16000

Perfect score: 1001
Sequence: 1 gcctaaaaattccccgtgtt.......ccctccccactggagaa 1001
                                                                                                                              March 30, 2003, 13:12:08 ; Search time 75.7689 Seconds
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/cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-10-032-393-47
US-10-032-393-8
US-10-032-393-8
US-10-078-090-83
US-10-012-542-44
US-10-012-542-44
US-09-960-352-382
US-10-102-866-28
US-10-102-866-28
US-10-102-866-38
US-09-960-352-14543
US-10-001-887-14
US-10-001-887-14
US-09-966-352-14268
US-09-966-352-14268
US-10-147-026-11
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Maximum Match 100%
Listing first 45 summaries
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Score 871.8; DB 10; Length 2907; Pred. No. 2.9e-211; 0; Mismatches 52; Indels 0;

Clark, Hilary Fechtel, Kim

APPLICANT

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                               CCCGCCAGGCAGCTGTAGCCCCAGCCTCAGCCCCAGCTCCAACAGAAGCAGCCCGGCCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCTTCCCCTCCCTCCACTGGAGAA 1001
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                                                                             POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
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                                                                                                                                                                                                                                                                 DB 10;
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APPLICANT: Agostino, Michael J.
APPLICANT: Howes, Steven H.
APPLICANT: Resnick, Richard J.
APPLICANT: Gulukota, Ramalakar
APPLICANT: Graham, James R.
TILE OF INVENTION: POLYNUCLEOTIDES ENCODING
FILE REFERENCE: GIN 6402
CURRENT APPLICATION NUMBER: US/09/822,830A
CURRENT FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/195,604
PRIOR APPLICATION NUMBER: 60/195,604
PRIOR APPLICATION NUMBER: 60/195,604
NUMBER OF SEO ID NOS: 631
SOFTWARE: PATENTING ONCY: 631
                                                                                                                                                                                                                                                                     100.0%; Pred. No.
                                                                                                                                                                                                                                                                 Score 578;
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Sub-10-184-644-346/c
; Sequence 346, Application US/10184644
; Publication No. US20030044930A1
; GENERAL INPORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 578; Conservative
                                                                                                                                                                                                                           sapiens
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                                                                                                                                                                                                                        ) ORGANISM: HOMO
US-09-822-830A-614
                                                                                                                                                                                  SEQ ID NO 614
LENGTH: 595
                                                                                                                                                                                                             TYPE: DNA
                                                                                                                                                                                                                                                                 Query Match
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Publication No. US20030027286A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Wall, Daniel
APPLICANT: Gross, Molly
TITLE OF INVENTION: BATERIAL PROMOTERS AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5.2%; Score 52.2; DB 9; 1
42.9%; Pred. No. 0.0057;
tlve 0; Mismatches 148;
                   CURRENT FILING DATE: 2011-12-21;
PRIOR APPLICATION NUMBER: 60/259,434
PRIOR FILING DATE: 2000-12-27
; PRIOR FILING DATE: 2000-12-27
; PRIOR FILING DATE: 2001-09-06
; PRIOR FILING DATE: 2001-09-06
; PRIOR FILING DATE: 2001-09-06
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PASISED for Windows Version 4.0
; SEQ ID NO 47
CURRENT APPLICATION NUMBER: US/10/032,393
CURRENT FILING DATE: 2001-12-21
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/032,393
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 60/259,434
PRIOR FILING DATE: 2000-12-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 09/948, 993
PRIOR FILING DATE: 2001-09-06
PRIOR PELICATION NUMBER: 60/230, 335
PRIOR FILING DATE: 2000-09-06
                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Vector peper14
US-10-032-393-47
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                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 42.99
Matches 111; Conservative
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Best Local Similarity
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                         APPLICANT:
APPLICANT:
APPLICANT:
Ban,James
APPLICANT:
Smith, Victoria
APPLICANT:
Matanabe,Colin K.
APPLICANT:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Wall, Daniel
APPLICANT: Gross, Molly
TITLE OF INVENTION: BACTERIAL PROMOTERS AND METHODS OF USE
FILE REFERENCE: ELITRA 010A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-032-393-47/c Sequence 47, Application US/10032393 Publication No. US20030027286A1 GENERAL INFORMATION:
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     Goddard, Audrey
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TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Gene FILE REFERENCE: DEX.0312
CURRENT APPLICATION NUMBER: US/10/078,090
CURRENT FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: 60/268,999
PRIOR FILING DATE: 2001-02-15
NUMBER OF SEQ ID NOS: 210
SOFTWARE: Patentin version 3.1
SEQ ID NO 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    761 AATITICATITIAAGCACATITATACIGAAGGAATITGIGCIGIGIATIGGGGGAGCIG 820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICAMT: Ruben et al.

TITLE OF INVENTION: 94 Human Secreted Proteins
FILE REFERENCE: P20291
CURRENT APPLICATION UNMER: US/10/012,542
CURRENT FILING DATE: 2001-12-12
PRIOR APPLICATION UNMER: EARLIER PELICATION NUMBER: 09/461,325
PRIOR PELICATION NUMBER: EARLIER PELICATION NUMBER: 09/61,325
PRIOR PELICATION NUMBER: EARLIER PELICATION NUMBER: 60/089,507
PRIOR PELICATION NUMBER: EARLIER PELICATION NUMBER: 60/089,507
PRIOR APPLICATION NUMBER: EARLIER PELICATION NUMBER: 60/089,507
PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
PRIOR FILING DATE: EARLIER PILING DATE: 1998-06-16
PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
PRIOR PELING DATE: EARLIER FILING DATE: 1998-06-12
PRIOR PELING DATE: EARLIER FILING DATE: 1998-06-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 954;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 48.2; DB 9; Length 9
Pred. No. 0.015;
0; Mismatches 73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              821 GATCCAGAGCTGGAGGGGGTGGGTCCGGGGGAGGGAGTGGCTCGG 865
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; Sequence 44, Application US/10012542
; Publication No. US20030044851A1
; GENERAL INFORMATION:
                                                                                                                                     Hu, Ping
Recipon, Herve
Karra, Kalpana
Cafferkey, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.8%;
                             Publication No. US20030044015.
GENERAL INFORMATION:
APPLICANT: Saleda, Susana
APPLICANT: Macina, Roberto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 55.8
Matches 92; Conservative
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SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                    Sun, Yongming
Liu, Chenghua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
CORGANISM: Homo sapien
US-10-078-090-83
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; ORGANISM: Homo sapiens
US-10-012-542-44
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APPLICANT:
APPLICANT:
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Patent No. US2002016433041
GENERAL INFORMATION:
APPLICART: Pan, Yang
TITLE OF INVERTION: AND USES THEREOF
FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/10/095,407
CURRENT FILING DATE: 1990-03-11
PRIOR APPLICATION NUMBER: US 60/091,650
PRIOR APPLICATION NUMBER: US 60/091,650
PRIOR PELING DATE: 1997-08-04
PRIOR FILING DATE: 1997-08-04
SPIOR FILING DATE: 1997-08-04
SOFTWARE: FastERQ for Windows Version 3.0
                                                                                         132 GCCCCCCCCCCCAGGCAGCTGTAGCCCCCAGCCTCAGCCCCCAGCTCCAACAGAAGAAGCAGCCCG 191
                                                                                                                                                                                                                                    192 GCCACCCACTCCCGGTGACCGCCCACGATGGACACAGCCCTCGCCCTCCGCCCGG 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             193 CCACCCACTCCCCGTGACCGCCCACGCCACATGGACACAGCCCTCGCCCTCCGCCCCGGC 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            253 TITICICIGCCITICIACCGACCATGIGACCCCGCACCAGCCCIGCCCCACCTGCCCTC 312
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       Mismatches 148; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 4.9%; Score 48.8; DB 9;
Best Local Similarity 52.5%; Pred. No. 0.15;
Matches 107; Conservative 0; Mismatches 97;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LOCATION: (1)...(152331)
; OTHER INFORMATION: n = A,T,C or G
US-10-095-407-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4509 CCCCCCACTTCAAAGGAC 4491
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  Conservative
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LOCATION: (1)...(15233.
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US-10-095-407-16
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US-10-078-090-83
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Matches
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Sequence 3882, Application US/09960352
Patent No. US20020137139A1
Batent No. US20020137139A1
Batent No. US20020137139A1
Batent No. US20020137139A1
BAPLICANT: Warren, Wesley C.
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: With alagam, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 3882
LENGTH: 266
252 CITITCICTGCCITICTACCGACCATGIGACCCCGCACCAGCCCTGCCCCCACCTGCCCT 311
                   83 CCCCGCCCCCCACACCCCCCGGGCCCCCCCAAAAAACCGCCTCCCCCCCAAAAAACCGC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   249 CGGCTTTTCTCTGCCTTTCTACGACCATGTGACCCCGCACCAGCCCTGCCCCACCTGC 308
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US-101-02-806-28/c
Sequence 28 Application US/10102806
Publication No. US20030054421A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA103PIC1
CURRENT APPLICATION NUMBER: US/10/102,806
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: BOS taurus
; OTHER INFERMATION: Clone ID: 17-LIB3058-036-01-K1-E1
US-09-960-352-3882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.4%; Score 44.4; DB 10;
43.9%; Pred. No. 0.07;
ilve 0; Mismatches 136;
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PRIOR APPLICATION NUMBER: 09/925,298
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/USO0/05881
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 846
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Matches 108; Conservative
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US-09-960-352-3882
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748 CCC 750
                                                                     CCC 314
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                                                                       761 AATITICATITIAAGCACATITATACIGAAGGAAITIGIGCIGIGIAITGGGGGGAGCIG 820
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681, 687, 691,
735, 739, 743,
847, 852
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                                                                                                                                                                                                                                                                                                                              Sequence 29, Application US/09804682
Patent No. US20020106765A1
Patent No. US20020106765A1
APPLICANT: INFORMATION:
APPLICANT: Corey, Michael J.
APPLICANT: BALONING THE SAME AND METHODS FOR SCREENING FOR CURRENT APPLICATION NUMBER: US/09/804,682
CURRENT PELLING DATE: 2001-03-12
NUMBER OF SEQ ID NOS: 174
APPLICANT: AND APPLICANT OF MINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LOCATION: 858, 878, 884, 886, 896, 897, 901, 917, 926, 932, 939, 948, LOCATION: 957, 961, 965, 981, 991, 993, 1001, 1002, 1005, 1011, 1018, LOCATION: 1043, 1047, 1049, 1051, 1054, 1056

US-09-804-682-29
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                                                                                                                                                                                                             DB 9; Length 569;
 4.6%; Score 40; 54.0%; Pred. No. 0.041; +ive 0; Mismatches 80; Indels
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674,
734,
823,
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Similarity 39.5%; Pred. No. 0.081;
96; Conservative 0; Mismatches 147;
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654,
731,
821,
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LOCATION: 485, 487, 488, 494, 496, 499, 511,
LOCATION: 583, 600, 611, 613, 623, 624, 652,
LOCATION: 594, 701, 713, 716, 720, 721, 725,
LOCATION: 744, 781, 782, 785, 789, 789, 803,
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: 5, 6, 16, 21, 24, 25, 33, 39,
LOCATION: 235, 237, 238, 244, 245, 246,
LOCATION: 321, 323, 330, 334, 340, 349,
LOCATION: 397, 405, 432, 437, 454, 455,
OTHER INFORMATION: n = A,T,C or G
                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: 858, 878, 884
LOCATION: 957, 961, 965
                   Similarity
                                       94;
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US-09-804-682-29
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LENGTH: 1064
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       Query Match
                          Local
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                       Best Loca
Matches
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Matches
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APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes
FILE REFERENCE: DEX-0269
CURRENT PILING DATE: 2001-11-20
PRIOR PILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-20
NUMBER OF SEQ ID NOS: 137
SOFTWARE: Patentin version 3.1
                                                                                                              GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298).C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 13784
LENGTH: 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          737 ITTTGTTTTGATTTTTAATAAGAATTTTCATTTTAAGCACATTTATACTGAAGGAATT 796
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: BOS taurus
; OTHER INCRMATION: Clone ID: 59-LIB3057-006-Q1-K1-G4
US-09-960-352-13784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 44; DB 10;
Pred. No. 0.11;
0; Mismatches 25
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                                                          Sequence 13784, Application US/09960352 Patent No. US20020137139A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 14, Application US/10001887 Patent No. US20020155464A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     761 AATTTTCATTTTAAGCACATTTAT 784
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Cafferkey, Robert
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Matches 77; Conservative
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Best Local Similarity
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                                   US-09-960-352-13784
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US-10-001-887-14
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APPLICANT:
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APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Fao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathalagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
TITLE OF INVENTION OF STORM OF 
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Pred. No. 0.16;
0; Mismatches 101; Indels: 0
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63.0%; Pred. No. 0.083;
1.ve 0; Mismatches 40; Indels
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US-09-960-352-14543
                                                                                                                                                                                                                                         OTHER INFORMATION: n equals a,t,g, or c, NAME/KEY: misc_feature
LOCATION: (1312)
OTHER INFORMATION: n equals a,t,g, or c, NAME/KEY: misc_feature
LOCATION: (1312)
OTHER INFORMATION: n equals a,t,g, or c, US-10-102-806-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 14543, Application US/09960352; Patent No. US20020137139A1
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Best Local Similarity 51.05
Matches 105; Conservative
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                 FEATURE: NAME/KEY: misc_feature LOCATION: (1311)
                                                                                                                 ORGANISM: Homo saptens
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US-09-960-352-14543
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RESULT 15

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U.S.-0-25-301-392/c

Sequence 392, Application Us/09925301

SEQUENCE TILE OF THE PRICENTION UNICLEIC. Acids, Proteins and Antibodies

FILE REPERBACE: PA106

CURRENT PELICATION WHERE: 020/09/925,301

PRIOR PELICATION WHERE: 2001-08-10

PRIOR APPLICATION WHERE: PCT/US00/05802

PRIOR FILING DATE: 1099-03-12

PRIOR FILING DATE: 1299-03-12

NUMBER OF SED ID NOS: 1694

SED ID NO 392

ILENCTH: 1545

TYPE: DAT

ORGANISM: Homo sapiens

FATURE: NAME/KEY: misc.feature

LOCATION: (34)

OTHER INFORMATION: n equals a,t,g, or c

LOCATION: (54)

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1420 TCTACAAAACCAGGAGGCCCTGCCCGCAGAGGCA 1385

Search completed: March 30, 2003, 16:47:31 Job time : 150.769 secs

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Catarrhini; Hominidae; Homo.

I (bases 1 to 1667)

National institutes of Health, Mammalian Gene Collection (MGC)

National institutes of Health, Mammalian Gene Collection (MGC)

National institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: DCTD/Drp

CDNA Library Preparation: Rubin Laboratory

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arayeb by: The I. M.A.G. E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be http://image.llnl.gov

Plate: LLCM2018 row: m column: 10

High quality sequence stop: 597.

Ince 1.1067
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A1401587 4928h01.x
A1640571 wa15408.x
AM130149 xf29a07.x
A8811759 ob80f09.s
AA670427 ad20g01.s
AA670427 ad20g01.s
AA670427 ad20g01.s
AA595224 n184f04.s
AR595224 n184f04.s
AR595224 n084f08.x
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AR595224 n184f04.s
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AR595234 TCAAP2D14
AL005074 ou08f08.x
BR747137 602020915
A1218536 q144b5.x
AM104216 x471100.x
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DEFINITION
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AUTHORS
TITLE
JOURNAL
COMMENT
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12561.622 Million cell updates/sec
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    GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                        16154066 seqs, 8097743376 residues
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                                                                             nucleic search, using sw model
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BM927280
BM554172
BM722189
AI806984
BQ044936
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/organism="Homo saplens"

/db.ref="taxon:9606"
/clone="INAGE:5517105"
/clone=IN=NIH_MGE:5517105"
/tissue_type="amelanotic melanoma, cell line"
/tissue_type="amelanotic melanoma, cell line"
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/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
/note="Organ: skin; Vector: poTB7; Site_1: Site_2: GGCACGAG(G): Library; constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a
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/lab_host="DH10B"
//lab_host="DH10B"
//lab_host="DH10B"
//note="Organ: brain; Vector: pCMV-SPORT6; Site_1": NotI;
Site_2" EcoRV (destroyed); RNA source anonymous pool of 3
fetal brains, female age 20 weeks, female age 24 weeks,
and male age 26 weeks. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
0.7-3:5 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 017. Note:
this is a NIH_MCC Library."
   sapiens cDNA clone IMAGE:5768263
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleoston
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1091)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 250
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                                                                                                                                                                                                                                                          Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can http://image.llnl.gov
http://image.llnl.gov
Plate: LLANL287 row, n column: 08
High quality sequence stop: 621.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5768263"
/clone_lib="NIH_MGC_121"
AGENCOURT_6688389 NIH_MGC_121
                 5', mRNA sequence.
BM927280
BM927280.1 GI:19377659
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="IMAGE:5469285"
/clone="IMAGE:5469285"
/tissue_type="amelanotic melanoma, cell line"
/tab_host="hull08 (phage-resistant)"
/note="Organ: skin; Vector: pOTB7; Site_1: xho!; Site_2: ECORI; cDNA made by oligo-dT priming. Directionally cloned into ECORI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZaP-cDNA synthesis kit (Stratagene) and
                                                                                                                                                                                                                                                                                                                                                                            BMS54172 1160 bp mRNA linear EST 20-FEB-2002 AGENCOURT_6581002 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5469285 5', mRNA sequence.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                   670
                                                                                                                                                                                               790
                                                                                                                                               730
                                                                                                                                                                       602
                                                                                                                                                                                                                                                  Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library." 324 c 280 g 219 t 164 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 1160)
NIH-MGC http://mgc.nci.nih.gov/.
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Prourement: DCTD/DTP
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CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CNA Sequencing by: Agencourt Bloscience Corporation
Clone distribution: MC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLCM1974 row: d column: 22
High quality sequence stop: 593.
Location/Qualifiers
                                                                                     CTGTACATACCCTGCCATACCAACCCCAGGTATTAATTCTCGCTGGTTTTGTTTTTATTT
                                                                                                                                                  TAATTTTTTTTTTTTTTTAATAAGAATTTTCATTTAAGCACATTTATACTGAA
                                                                                                                                                                                                  791 GGAATITGTGCTGTGTATTGGGGGG--AGCTGGATCCAGAGCTGGAGGGGGTGGGTCCGG
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BM722189 654 bp mRNA linear EST 01-MAR-2002
UI-E-E00-ahy-m-11-0-UI.rl UI-E-E00 Homo sapiens cDNA clone
UI-E-E00-ahy-m-11-0-UI 5', mRNA sequence.
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l; Hominidae; Homo.
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1 (bases 1 to 654)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                     342
                                                                                           343 ACGGGGAGGAGGAGGCAGCGACTCCTTGGACAGAGGCCTGGGGCCTCAGTGGACTGCCT 402
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                                                                                                        TCACCACATCTTCATCACCAGCAAACGCCAGGACTTGGCTCCCCCATCCTCAGAACTCAC
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             .7e-105;
67.6%; Score 676.4;
97.8%; Pred. No. 3.7e
iive 0; Mismatches
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BM722189.1 GI:19042595
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TITLE
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/db_xref="taxon:9606"
/clone="Ul=E00-aby-m-11-0-UI"
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                                                                                                                                                                                                                                                                          Email: msoarces@blue.weeg.ulowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Glone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
The following repetitive elements were found in this CDNA
sequence: 407-459, AT_rich#Low_complexity
Seq primer: M13 Reverse.
                                                                                                                                                    University of Iowa
451 Ecstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
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1larity 99.5%; Pred. No. 8.3e-101;
Conservative 0; Mismatches 3;
discovery
Genome Res. 6 (9), 791-806 (1996)
                                                                                                                         Discovery
                                                                                       Contact: Soares, MB
Program for Rat Gene
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EST 18-DEC-1999
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 703)
NCI-CAAP http://www.ncbi.nlm.nlh.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs remail.nih.gov
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
TNAGE Consortium (info@image.llnl.gov) for further, information.
Insert Length: 794 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 469.
Location/Qualifiers
1. 703
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                            420
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                                                                           TIGTGCTGTGTATTGGGGGGAGCTGGATCCAGAGCTGGAGGGGGTGGGGGTCCGGGGGAGGG
                                                                                                                                                                                                 676 CATACCCTGCCATACCAACCCCAGGTATTAATTCTCGCTGGTTTTGTTTTTAATT
              AGTGGCTCGGAAGGGGCCCCCACTCTCCTTTCATGTCCCTGTGCCCCCCAGTTCTCCTCC
                                                           TITITIGITITIGATITITIAATAAGAATITITCATITITAAGCACATITIATACTGAAGGAAT
                                                                                                                                                                                                                                               916 TCAGCCITITCCTCCTCAGTITTCTCTTTAAAACTGTGAAGTACTAACTTTCCA 969
                                                                                                                                                                                                                                                                              601 TCAGCCTTTTCCTCCTCAGTTTTCTCTTTANNACTGTGAAGTACTTTCCA 654
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/lab_host="DH10B"
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240 g 133 t
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Pred. No. 1.6e-99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                        AI806984
AI806984.1 GI:5393550
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184 c
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98.8%;
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COMMENT
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Unpublished (1997).

Contact: Robert Strausberg, Ph.D.

Email: cgapbs.r@mail.nih.gov

Tissue Procurement: Dr. Jose Mercuende

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: http://image.lln.gov

sequence: 1-73, >AT_rich#Low_complexity (matched compliment)

Seq primer: MI3 FORWARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 654)
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                               250
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UI-H:EUO-azo-e-05-0-UI.SI NCI_CGAP_Carl Homo sapiens cDNA clone
IMAGE:5851372 3', mRNA sequence.
                                                                                                                       310
                                                                                                                                                 476
                                                                                                                                                                                                                                    430
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GGCCCCCCCCAGGCAGCTGTAGCCCCAGCCTCAGCCCCAGCTCCAACAGAAGCAGCCC
              GGCCACCCACTCCCCGTGACCGCCCACGCCACGCCACGGCCTCGCCCTCCGCCCCG
                                                                     GCTTTTCTCTGCCTTTCTACCGACCATGTGACCCCGCACCAGCCCTGCCCCACCTGCCC
                                                                                                                             TCCCGGGCAGTACTGGGGACCTTCCCTGGGGGACGGGGAGGAGGAGGCAGCGACTCCTT
                                                                                                                                                                                                                         GGACAGAGGCCTGGGCCCTCAGTGGACTGCCTGCTCCCACAGGCTGGGCTGACGTCAGAG
                                                                                                                                                                                                                                                                                                                                                      GCCGAGGCCAGGAACTGAGTGAGGCCCCTGGTCCTGGGTCTCAGGATGGGTCCTGGGGGC
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BQ044936/c
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DEFINITION
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/clone="Inda@E:581372"
/clone="Ibb"NCI_CGAP_Carl"
/tlosue_type="Osteoarthritic Cartilage"
/fusue_type="Osteoarthritic Cartilage"
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/lab_host="DH10B (Life Technologies)"
/note="Organ: Knee; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I: Site_2: Not I;
NCI_CGAP_Carl is a cDNA library containing the following tissue(s): Osteoarthritic Cartilage The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oilgo-dry primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I into pT713-Pac vector. The oilgonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the mannancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 639.6; DB 14; Length 654;
Pred. No. 7.1e-99;
0; Mismatches 9; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                             TAG_TISSUE-osteoarthritic cartilage
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                                                                                                                                                                                                                                                                                                                                                                                                                                 131
                                            /organism="Homo sapiens'
                                                            /db_xref="taxon:9606
                .on/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                             TAG_SEQ-TGATCACGCT"
161 c 227 q
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il Similarity 98.6%;
645; Conservative
POLYA-Yes
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/lab_host="DH10B"
/lab_host="DH10B"
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67 a 293 c 331 g 177 t 10 others
                                                                                                                                                                                                                                                                                                                                                                                                                                AL522712 LTI_NFL004_NBC2 Homo sapiens cDNA clone CS0DB009YG04 3 prime, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 978)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
                                                  728
                                                                                    420
                                                                                                                     788
                                                                                                                                                       480
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                                                                                                                                                                                                   Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr.
                                                 CCCTGTACATACCCTGCCATACCAACCCCAGGTATTAATTCTCGCTGGTTTTGTTTTAT
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/organism="Homo sapiens"
/ob_xref="taxon:9606"
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/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 60.2%; Score 602.6; Best Local Similarity 90.9%; Pred. No. 1.2e Matches 613; Conservative 5; Mismatches
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TITLE
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                                                                                                                                  mRNA linear EST 24-MAY-2002 sapiens cDNA clone IMAGE:6018014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Romo saplens"
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/tissue_type="Eptthelioid carcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT. Perchonlogies."
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S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Tissue Procurement: ArG.

CDNA Library Preparation: Life Technologies, Inc.

COND CONSTILUTION: MGC Clone distribution information can be http://image.lnl.gov

Plate: LLAM13218 row: d column: 15

High quality sequence stop: 563.

Location/Qualifiers

rece 1.: (bases 1 to 954)

Location/Conalifiers

Free 1.: (bases 1 to 954)

Location/Conalifiers

Free 1.: (bases 1 to 954)

Location/Conalifiers
                                                                                                                                                                                                                                                                     Euteleostom1;
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Pred. No. 4.8e-97;
0; Mismatches 10
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AGENCOURT_7761844 NIH_MGC_70 Homo
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298 c
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Best Local Similarity 98.4%;
Matches 634; Conservative
                                                                                                                                                               , mRNA sequence.
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bp mRNA linear EST 13-FEB-2001 sapiens cDNA clone CSODN004Y122 5
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Homo.
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CCCGCCAGGCAGCTGTAGCCCCAGCCTCAGCCCCAGCTCCAACAGAAGCAGCCCGGCCAC
                                         CCACTCCCCGTGACCGCCCACATGGACACAGCCCTCGCCCTCGGCCCCGGCTTTT
                                                                               GCAGTÀCTGGGGACCTTCCCTGGGGGACGGGAGGGAGGAGGCAGCGACTCCTTGGACAG
                                                                                                                                  AGGCCTGGGCCCTCAGTGGACTGCCTGCTCCCACAGCCTGGGCTGACGTCAGAGGCCGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; En
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; I
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="CSODNO04Y122"
/clone_lib="LTI_FL015_Brn1"
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/db_xref="taxon:9606"
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AL533351 LTI_FL015_Brn1 Homo
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/tissue_type="Adult brain"
/note="Vector: pCMVSPORT 6; Site_1: Not!; Ist strand cDNA was primed with a Not!-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland flang@lifetech.com URL:

http://fulllength.invitrogen.com"

325 c 286 g 177 t 6 others
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                                                                                                                                              Score 599; DB 9; Length 967; Pred. No. 4.9e-92;
                                                                                                                                                                    Indels
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                                                                                                                                                                   Mismatches
                                                                                                                                                                  5.
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|||||| ||||||||||||
TTTTTTTTTGATTTTTTAWT 967
                                                                                                                                             59.8%;
                                                                                                                                                                  Conservative
                                                                                                                                                        Similarity
                                                                                                                                                                621;
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                                                                                                                                                         Local
                                                                                                                                                               Matches
                                                                                                             BASE COUNT
ORIGIN
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734

78

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/organism="Homo saplens"
/dry refe"taxon:9606"
/clone_iDp="LTI_NELO6_PL2"
/clone_iDp="TI_NELO6_PL2"
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/close_type="Placenta"
/cloned with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, maryland 20850, USA Fax: (1) 301 610 8371
                                                                                                                                                                                                                                                                                                      993 bp mRNA linear EST 16-FEB-2001
Homo sapiens cDNA clone CSODI066YK12 3
                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (Dases 1 to 993)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length CDNA libraries and normalization
Contact: Genoscope
   : www.genoscope.cns.fr.
                                                                   675 ACATACCCTGCCATACCAACCCCAGGTATTAATTCTCGCTGGTTTTGTTTTTTTAAT
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BP 191 9106 EVRY cedex - France
Email: Seqrefégenoscope.cns.fr, Web : www.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
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prime, mRNA sequence.
AL551103
AL551103.1 GI:12888727
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Best Local Similarity
Matches 619; Conserva
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AL551103/c
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                      197
                                                                                   137
                                                                                                                                                   11
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TITLE
JOURNAL
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/iasue_type="neuroblastoma cells"
/iab_host="DH10B"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-ollgo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by Life Technologies. Contact: Feng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax: (1) 301 610
8371 Email: filang@lifetech.com URL:
http://fulllength.invitrogen.com"
275 c 316 g 172 t 2 others
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                                                                 Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                             Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cons. France
Bmail: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
1. 931
| /organism="Homo sapiens"
/db_xref="taxon:9606"
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Lt,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 59.7%; Score 597.8; DB 9; Best Local Similarity 92.0%; Pred. No. 7.8e-92; Matches 621; Conservative 0; Mismatches 52;
                                                                                                                                                                                                                                                                                               /clone="CSODMO01YN13"
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/sex="male"
   GI:12794642
                                                  Homo sapiens
   AL531149.1
                                                ORGANISM
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TITLE
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A1963441 626 bp mRNA linear EST 20-AUG-1999 wt63c08.xl NCI_CGAP_Pan1 Homo sapiens cDNA clone INAGE:2512142 3' similar to 9b:M/3779 RETINOIC ACID RECEPTOR ALPHA-1 (HUMAN);, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Life Technologies catalog #: 11548-013
DNA. Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 409.
Location/Qualifiers
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 692)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
    catalog
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Average insert size 1.72 kb. Life Technologies 11548-013" 3 others
                                                                      5;
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                                                 Score 593.8; DB 9;
Pred. No. 4.1e-91;
); Mismatches 5;
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Contact: Robert Strausberg, Ph.D.
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llarity 98.9%;
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AA812217/c
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/clone_lib="LTI_NEUTO6_PL2"
/tissue_type="placenta"
/flote=lib="LTI_NEUTO6_PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_l: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fullength.invitrogen.com"
89 a 311 c 354 g 189 t 8 others
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Catarrhini; Hominidae; Homo.
      137 CCCGCCAGGCAGCTGTAGCCCCCAGCCTCAGCTCCAACAGAAGCAGCCGGGCCAC 196
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GENOSCOPE - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
                                                                   119 CCTGTACATACCCTGCCATACCAACCCCAGGTATTAATTCTCGCTGGTTTTGTTTTATT
                                                   670 CCTGTACATACCCTGCCATACCAACCCCAGGTATTAATTCTCGCTGGTTTTGTTTTATT
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Bukaryota; Metazoa; Chordata; Craniata; Verte
Bukaryota; Butheria; Primates; Catarrhini; Hon
1 (bases 1 to 1051)
Lii,W.B., Gruber,C., Jessee,J. and Polayes,D.
Unpublished (2001)
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Pred. No. 2.2e-90;
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/db_xref="taxon:9606"
/clone="CSODK004YG05"
                                                                                                                                                                                                                                 1051
Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
1. .1051
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prime, mRNA sequence.
AL578663
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90.0%;
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                                                                                               Sequencing Center
information can be
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       131 GGCCCCCCCCCCAGCAGCTGTAGCCCCAGCCTCAGCCCCAACAGAAGCAGCCC 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 692;
                                                                      CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome :
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40ml3 fwd. Er from Amersham
High quality sequence stop: 469.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                     /clone="IMAGE:1338100"
/clone_lib="NCI_CGAP_GCB1"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 590.8; DB 9;
Pred. No. 1.3e-90;
0; Mismatches 14;
                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 59.0%;
Best Local Similarity 97.2%;
Matches 632; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 602)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tumor Gene Index
Unpublished (1997)
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs.r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40Up from glaco
High quality sequence stop: 468.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                              74
                                                                                                                                                                                                                                                                                                                                                                                                                                                            73 TAACCCEGCCATACCAACCCCAGGTATTAATTCTCGCTGGTTTTGTTTTAATTT 14
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IMAGE:2605546 3' similar to gb:M73779 RETINOIC ACID RECEPTOR
ALPHA-1 (HUMAN);contains element MSR1 repetitive element ;, m
                                                                             AGGCCTGGGCCCTCAGTGGACTGCCTGCTCCCACAGCCTGGGCTGACGTCAGAGGCCGAG
                                                                                                                                    GCCAGGAACTGAGTGAGGCCCCTGGTCCTGGGTCTCAGGATGGGTCCTGGGGGCCTCGTG
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/db_xref="taxon:9606"
/clone="inAdE:2605546"
/clone=lib="Soares_NFL_T_GBC_S1"
/lab_host-"DH108"
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682632-687239,
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                                                                                      243 CCGCCCGGCTTTTCTCTGCCTTTCTACCGACCATGTGACCCCGGCACCAGCCCTGCCCCC
                                                                                                                    CGTCAGAGGCCGAGGCCAGGAACTGAGTGAGGCCCCTGGTCCTGGGTCTCAGGATGGGTC
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                                                                                                                                          GCAAACGCCAGGACTTGGCTCCCCCATCCTCAGAACTCACAAGCCATTGCTCCCCAGCTG
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                                                                                                                                                                                                                                                                                                                                     ij
     I.M.A.G.E. clones 297480-302087, 682632-687239
726408-728711, and 729096-731399. Subtraction
Soares and M. Fatima Bonaldo. " 1 others
15 c 203 g 109 t 1 others
                                                    Length 602;
                                                 Score 572.8; DB 10; Length
Pred. No. 1.5e-87;
0; Mismatches 8; Indels
                                                 57.2%;
98.5%;
                                                                 588; Conservative
                                                         Similarity
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                                                 Query Match
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completed: March 30, 2003, 13:48:36 le : 1300.57 secs Search

time

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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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model OM nucleic - nucleic search, using sw March 29, 2003, 14:38:45; search time 158 Seconds (without alignments) 11234.997 Million cell updates/sec Run on:

US-09-691-220-1 2086 Perfect score: Sequence:

Scoring table:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0

Total number of hits satisfying chosen parameters: 574371 seqs, 425486471 residues Searched:

1148742

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

/cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	Cadional Sol	Sequence 1 Appli	Segment 7 Appli	م			7	Sequence 5714. An	Segmence 12806. A		Sequence 4521 An		Sequence 2138. Ap		26.	29	1197		121
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SUMMARIES	QI Q	US-09-954-456-524	US-09-797-727-1	US-10-239-804-7	US-10-239-804-8	US-10-239-804-9	US-10-239-804-10	US-09-822-830A-614	US-09-960-352-5714	US-09-960-352-12806	US-09-960-352-31	US-09-960-352-4521	US-09-833-381-92	US-09-960-352-2138	US-09-962-436-567	US-09-965-703-26	US-09-965-703-62	US-09-833-381-1197	US-09-965-703-21	US-09-833-381-1210
	DB	10	10	σ	σ	σ	6	10	10	10	10	10	10	10	10	10	9	10	10	10
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dp	Query Match	85.3	35.9	33.6	33.6	33.6	33.6	28.4	18.0	18.0	17.4	17.4	15.6	13.5	9.8	8.4	8.4	8.3	8.3	8.2
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Sequence 22, Appl Sequence 37, Appl Sequence 59, Appl Sequence 1, Appl Sequence 1, Appli Sequence 1, Appli Sequence 109, App Sequence 109, App Sequence 45, Appl Sequence 47, Appl Sequence 47, Appl Sequence 1, Appl Sequence 1, Appl Sequence 316, App Sequence 316, App Sequence 316, App Sequence 310, App Sequence 310, App Sequence 41, Appl Sequence 41, Appl Sequence 421, Appl	36, A 1, Ap 1802, 28, A
US-09-921-650-22 US-09-921-650-37 US-09-91-650-37 US-09-909-446-1 US-09-909-325-1 US-09-909-325-1 US-09-909-326-1 US-09-909-326-1 US-09-96-326-1 US-09-96-326-1 US-09-96-326-1 US-09-96-326-1 US-09-96-326-1 US-09-96-326-1 US-09-96-336-89-1 US-09-96-44-090-316-1 US-09-96-4-4-090-316-1 US-09-96-4-4-090-316-1 US-09-96-4-4-090-316-1 US-09-96-4-4-090-316-1 US-09-96-4-4-0-1 US-09-96-4-4-0-1 US-09-96-4-4-0-1 US-09-96-4-4-0-1 US-09-96-4-4-0-1 US-09-96-4-4-0-1 US-09-96-4-4-0-1 US-09-96-4-4-0-1 US-09-96-4-4-0-1	US-09-919-497-36 US-09-895-840-1 US-09-960-352-1802 US-09-965-703-28
816 9 816 9 816 9 15948 9 109344 10 10934 10 10528 10 10528 10 10528 10 10538	111 10 56 10 57 10 50 10
816 816 118943 1189443 1193444 1193444 119344 11849 11	2511 2066 367 850
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ALIGNMENTS

US-09-954-456-524

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APPLICANT: Young, Paul
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using (
TITLE OF INVENTION: Sets
FILE REFERENCE: 689290-76
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Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2000-09-20
PRIOR PLILING DATE: 2000-09-20
PRIOR FILING DATE: 2000-09-25
PRIOR PLILING DATE: 2000-09-25
PRIOR PELICATION NUMBER: US/60/235,134
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,637
PRIOR PELICATION NUMBER: US/60/235,637
PRIOR PELICATION NUMBER: US/60/235,711
PRIOR PELICATION NUMBER: US/60/235,711
PRIOR PELING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/954,456
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: US/60/233,617
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US/60/234,052
Sequence 524, Application US/09954456 Patent No. US20020115057A1
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Best Local Similarity 99.3%;
Matches 1786; Conservative
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ORGANISM: Homo sapiens
                                                                  GENERAL INFORMATION:
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Patent No. US20020077457A1

GENERAL INFORMATION:
APPLICANT: The Salk Institute for Biological Studies APPLICANT: The Salk Institute for Biological Studies APPLICANT: TARAKU, Funimaro
TITLE OF INVENTION: GAMMA RETINOIC ACID RECEPTOR FILE REFERENCE: SALKI150-3
CURRENT APPLICATION NUMBER: US/09/797,727
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: US 08/486,325
PRIOR APPLICATION NUMBER: US 08/100,039
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1990-06-22
PRIOR PLILNG DATE: 1980-06-22
PRIOR PLILNG DATE: 1980-06-22
PRIOR PLILNG DATE: 1980-06-22
PRIOR FILING DATE: 1980-06-22
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Version 3.0
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LENGTH: 15
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SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 7
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OTHER INFORMATION:
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                                                                  Length 1577
                                                                Score 749.2; DB 10; Length
Pred. No. 9e-182;
0; Mismatches 223; Indels
              NAME, KEY: misc_feature
OTHER INFORMATION: Human Retinoic Acid I
NAME, KEY: CDS
LOCATION: (200)..(1576)
                                                                35.9%;
79.8%;
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ORGANISM: Human
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Pred. No. 1.6e-169;
0; Mismatches 248;
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/10239804

Publication No. US20030053991A1

GENERAL INFORMATION:

APPLICANT: Oxford Blomedica (UK) Limited

APPLICANT: Kingsman, Alan J

APPLICANT: Maden, Malcolm

APPLICANT: Corcoran, Jonathan PT

TITLE OF INVERTION: Factor

FILE REFERENCE: P009156WOCTH

CURRENT APPLICATION NUMBER: US/10/239,804

CURRENT FILING DATE: 2000-09-23

PRIOR FILING DATE: 2000-09-23

PRIOR RPLING DATE: 2000-09-30

PRIOR RPLING DATE: 2000-09-30

PRIOR FILING DATE: 2000-09-30

PRIOR FILING DATE: 2000-00-40

NUMBER OF SEQ ID NOS: 73
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ORGANISM: Artificial Seguence
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Best Local Similarity 77.4%;
Matches 850; Conservative
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Query Match
                       FEATURE:
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Matches
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GAGATGACAGCGGAGCTAGACGACCTCACTGAGAAGATCCGGAAAGCCCCACCACCAGCAGAAACC
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                                  TTCCCTGCCCTCTGCCAGCTGGGCAAATACACTACGAACAACAGCTCAGAACAACGTGTC
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| Publication No. US20030053991A1
| GENERAL INFORMATION:
| APPLICANT: Oxford Biomedica (UK) Limited
| APPLICANT: Mingsman, Alan J
| APPLICANT: Maden, Malcolm
| APPLICANT: Maden, Malcolm
| APPLICANT: Corcoran, Jonathan PT
| TILLE OF INVENTION: Factor
| FILE REFERENCE: PO09156WC-TH
| CURRENT FILING DATE: 2002-09-23
| PRIOR FILING DATE: 2000-03-30
| PRIOR FILING DATE: 2000-03-30
| PRIOR FILING DATE: 2000-03-30
| NUMBER OF SEQ ID NOS: 73
| SEQ ID NO 8
| SEQ ID NOS: 73
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                                  ; OTHER INFORMATION: Description of Artificial Sequence: FLAG RARbeta2; OTHER INFORMATION: PCR product US-10-239-804-8
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                                                                                   Score 701.2; DB 9;
Pred. No. 1.6e-169;
0; Mismatches 248;
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larity 77.4%;
Conservative 0
TYPE: DNA
ORGANISM: Artificial Sequence
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SOFTWARE: PE
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                                   1246 ATGAAGATTACTGACCTGCGAAGCATCAGCGCCAAGGGGGGCTGAGCGGGTGATCACGCTG 1305
                                                   AAGATGGAGATCCCGGGCTCCATGCCGCCTCTCATCCAGGAAATGTTGGAGAACTCAGAG 1365
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Pred. No. 4.6e-169;
0; Mismatches 248;
                                                                                                                                                                                                                                                                                                     APPLICANT: Kingsman, Alan J
APPLICANT: Maden, Malcolm
APPLICANT: Corcoran, Jonathan PT
TITLE OF INVENTION: Factor
FILE REFERENCE: P009156W0CTH
CURRENT FILING DATE: 2002-09-23
CURRENT FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: PCT/GB00/01211
PRIOR APPLICATION NUMBER: GB 0024300.6
PRIOR APPLICATION NUMBER: GB 0024300.6
PRIOR FILING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 9
                                                                                                                                                                                                                                                 Sequence 9, Application US/10239804
Publication No. US20030053991A1
GENERAL INFORMATION:
APPLICANT: Oxford Blomedica (UK) Limited
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 33.6%;
Best Local Similarity 77.4%;
Matches 850; Conservative (
                                                                                                                                                    GGCCTGGACACTCTGAGC 1383
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Publication No. US20030053991A1
GENERAL INFORMATION:
APPLICANT: Oxford Blomedica (UK) Limited
APPLICANT: Maden, Malcolm
APPLICANT: Corcoran, Jonathan PT
TITLE OF INVENTION: Factor
FILE REFERENCE: P009156WOCTH
CURRENT APPLICATION NUMBER: US/10/239,804
CURRENT APPLICATION NUMBER: DCT/GB00/01211
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PRIOR APPLICATION NUMBER: GB 0024300.6
PRIOR FILING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 73
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APPLICANT: Howes, Steven H.
APPLICANT: Howes, Steven H.
APPLICANT: Resnick, Richard J.
APPLICANT: Resnick, Rainalkar
APPLICANT: Graham, James R.
APPLICANT: Graham, James R.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
FILE REFERENCE: GIN 6402
CURRENT APPLICATION NUMBER: US/09/822,830A
CURRENT FILING DATE: 2001-03-29
PRIOR PAPLICATION NUMBER: 60/195,604
PRIOR FILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 631
                                    3978 ATGAAAATCACAGATCTCCGCAGCATCAGCGCGAAAGGTGCCGAACGTGTAATTACCTTG
                                                                             1306 AAGATGGAGATCCCGGGCTCCATGCCGCCTCTCATCCAGGAAATGTTGGAGAACTCAGAG
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                                                                                                                                                                                                                                          Sequence 614, Application US/09822830A Patent No. US20020142952A1
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APPLICANT: Wong, Gordon G.
APPLICANT: Clark, Hilary
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LENGTH: 595
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                                                                                         9151;
                             CTHER INFORMATION: Description of Artificial Sequence: CTHER INFORMATION: ponY-FLAG-RARbeta2 vector genome plasmid US-10-239-804-10
                                                                                          Length
                                                                                                                      Indels
                                                                                                                      0; Mismatches 248;
                                                                                         Score 701.2; DB 9;
Pred. No. 4.6e-169;
ORGANISM: Artificial Sequence FEATURE:
                                                                                       Query Match 33.6%;
Best Local Similarity 77.4%;
Matches 850; Conservative
                                                                                         Query Match
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RESULT 10
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                                                                                                                                                                               Sequence 5714, Application US/09960352

Patent No. US20020137139A1

GENERAL INFORMATION:

APPLICANT: Wasley C.

APPLICANT: Tao, Nengbing

APPLICANT: Byatt, John C.

APPLICANT: Mathialagan, Nagappan

APPLICANT: Mathialagan, Nagappan

ITILE OF INVENTION: MUSCLE AND FAT DEPOSITION

FILE REFERENCE: 16511.006/37-21(10298)C

CURRENT APPLICATION NUMBER: US/09/960,352

CURRENT FILING DATE: 2001-09-24

NUMBER OF SEQ ID NOS: 15112
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           536 ACTGCCGACTGCAGAAGTGCTTTGAAGTGGGCATGTCCAAGGAGTCTGTGAGAAACGACC 595
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596 GAAACAAGAAGAAGAAGGAGGTGCCCAAGCCCGAGTGCTCTGAGAGCTACACGCTGACGC
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Pred. No. 1.9e-86;
0; Mismatches 19; Indels 0;
                                                                                                             361 AGGCTGCCTGCATATCCTGATCCTGCGGATCTGCACGCGCTA 406
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CRGANISM: Bos taurus
CTHER INFORMATION: Clone ID: 25-LIB188-001-Q1-E1-G1
US-09-960-352-5714
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Sequence 12806, Application US/09960352
Patent No. US20020137139A1
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 18.0%;
Best Local Similarity 95:3%;
Matches 387; Conservative (
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US-09-960-352-5714
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Sequence 31, Application US/09960352
Patent No. US20020137139A1
Patent No. US20020137139A1
Patent No. US20020137139A1
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathalagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT PILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 31
                                                                                                                          MOLECULES ASSOCIATED WITH LACTATION AND
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                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Bos taurus
COTHER INFORMATION: Clone ID: 55-LIB188-005-Q1-E1-F4
US-09-960-352-12806
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; OTHER INFORMATION: Clone ID: 01-LIB188-009-Q1-E1-A1
US-09-960-352-31
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECUI
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REPERRENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ. ID NOS: 15112
SEC. D. 12806
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APPLICANT: Robison, Keith E.
TITLE OF INVENTION: No. US20020132090Alel Nucleic Acid and Protein Homologs
FILE REPERENCE: 5800-119
CURRENT APPLICATION NUMBER: US/09/833,381
CURRENT FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 09/516,448
PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 2050
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 92
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                                                                               TCTGCCAACTGGGCAAATACACTACGAACAACAGCTCAGAACAGCGTGTCTCTCTGGACA 240
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                          216 TGCTTTGGCCCCCTCAACGGACTTGTTTTGCTTTCCCAAACCAGCTGTGCCCCCTGGGG
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Pred. No. 2.3e-73;
0; Mismatches 44; I.
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Best Local Similarity 89.1%;
Matches 407; Conservative
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TYPE: DNA
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Patent No. US20020137139A1
GENERAL INFORMATION:
APPLICANT: Wasley C.
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Wathielagan, Nagappan
APPLICANT: Wathielagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 4521
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                             Gaps
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 DB 10; Length 429;
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Pred. No. 4e-83;
0; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                AAGGCTGCCTGCACATCCTGATCCTGCGGATCTGCACG 936
                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 20-LIB188-012-Q1-E1-E11
US-09-960-352-4521
              2.3e-83;
               Pred. No. 2.3e
0; Mismatches
 Score 363.6;
              Pred.
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17.4%;
94.0%;
                         Conservative
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            Similarity
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Best Local Similarity
            Best Local Sim
Matches 378;
Query Match
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DB 10; Length 2288;

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                                                                                                                     360 CATCTACAAGCCTTGCTTTGTCTGTCAGGACAAGTCCTCAGGCTACCACTATGGGGTCAG 419
                                                                                                                                       534 GTACTGCCGACTGCAGAAGTGCTTTGAAGTGGGCATGTCCAAGGAGTCTGTGAGAACGA
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                                                                         Pred. No. 1.4e-35;
0; Mismatches 474;
                                                            Score 178.6;
                                                         Watch 8.6%;
Local Similarity 51.3%;
nes 581; Conservative C
               Homo sapiens
           ; ORGANISM: HOM
US-09-962-436-567
                                                            Query Match
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TYPE:
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Patent No. US20020081301A1
GENERAL INFORMATION:
TUTUE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu TITLE OF INVENTION: Sets
FILE REPERENCE: 689290-75
CURRENT FILING DATE: 2001-09-25
CURRENT PILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
NUMBER OF SEQ ID NOS: 568
SSO ID NO 567
LENGTH: 2288
                                                                                                                    MOLECULES ASSOCIATED WITH LACTATION AND
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                                                                                                                                                                                                                                                                                                                                                                               Score 282.4; DB 10; Length 416;
Pred. No. 1.4e-62;
0; Mismatches 17; Indels 2;
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ACATCCTGATCCTGCGGATCTGCACGCGGTACA 943
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ilarity 94.3%;
Conservative C
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Best Local
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1270 ATCAGCGCCCAAGGGGGCTGAGCGGGTGATCACGCTGAAGATGGAGATCCCGGGCTCCATG 1329
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                                                  880 ArceGecreAAArGCCTGGAACATCTCTTCTTCAAGCTCATCGGGGACACACCCATT 939
                        793 TTCAGTGAACTCTCCACCAAGTGCATCATTAAGACTGTGGAGTTCGCCAAGCAGCTGCCC
                                                                                                                                 913 ATCCTGATCCTGCGGATCTGCACGCGGTACACGCCCGAGCAGGACACCATGACCTTCTCG
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Job time : 201 secs
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APPLICANT: Rohm and Haas Company
APPLICANT: Rohm and Haas Louba Reddy
APPLICANT: Rohm and Haas Louba Reddy
APPLICANT: Rohm and Haas Louba Reddy
APPLICANT: Cress, Dean Ervin
TITLE OF INVENTION: No. US20020119521Alel Ecdysone Receptor-Based Inducible Gene Expl
FILE REFERENCE: A01020B
CURRENT APPLICATION NUMBER: US/09/965,703
CURRENT FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-20
PRIOR APPLICATION NUMBER: 60/191,355
PRIOR APPLICATION NUMBER: E07/0501/09050
PRIOR FILING DATE: 2001-03-20
PRIOR FILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn version 3.1
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GAAAGTCGAGTGCCCCACCGAACTCTTCCCCCCACTCTTCCTCGAGGTCTTTGAGGATCA 1689
                                                               GAAGATGGAGATCC---CGGGCTCCATGCCGCCTCTCATCCAGGAAATGTTGGAGAACTC 1361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             733 TACACTACGAACAACAGCTCAGAACAACGTGTCTCTGGGACATTGACCTCTGGGACAAG 792
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                                                                                                                                              1690 GGAAGTCTAAAGCCTCAGGCGCCAGAGGCTGCGGAGGTGCGGAGGAG 1742
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY: misc_feature
; OTHER INFORMATION: No. US20020119521A1el Sequence
US-09-965-703-26
                                                                                                                                                                                                                                                                                               Sequence 26, Application US/09965703 Patent No. US20020119521A1 GENERAL INFORMATION:
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LENGTH: 1123
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                         GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                          OM nucleic · nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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A1806984 wf244908.x
B0708346 602295596
B17907041 603065004
AAB12217 00844903.s
B1914043 603179258
BE547412 601072989
B1891823 602779839
B1891832 602779839
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Query

Score Match Length DB ID

960.8 46.1 1051 9 AL538663 AL578663 AL578663 923.6 44.3 967 9 AL533351 AL533351 AL533351 AL553351 AL553392 903.6 44.3 978 9 AL52712 AL556392 AL568392 AL568392 AL568392 AL568392 AL568392 AL568384 AL568384 AGENCOURT

Result No.

AL578663 1051 bp mRNA linear EST 16-FEB-2001 AL578663 LTL.NFL006_PL2 Homo sapiens cDNA clone CSODK004YG05 3	prime, mRNA sequence. ALS78663	ATJ 8003.1 GI:12942534 EST. human.	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1051)	LI.W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization	Unpublished (2001)	Contact: Genoscope	Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France	<pre>Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr. Location/Oualifiers</pre>		/organism="Homo sapiens" /db xref="taxon:9606"	/clone="CSODK0041G05"	/clone_lib="LTI_NFL006_PL2"	/tissue_type="placenta"	<pre>/note="Vector: pCMVSPORT 6; Site_1: NotI; ist strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end</pre>	
RESULT 1 AL578663/c LOCUS DEFINITION	ACCESSION	VERSION KEYWORDS SOURCE	ORGANISM	REFERENCE	AUTHORS TITLE	JOURNAL	COMMENT		FEATURES	source						

ALIGNMENTS

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Homo sapiens
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Matches 956; Conserv
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enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pcMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologias. Contact: Feng Liang Life Technologies. Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: filliangelifetech.com, URL: http://fulliengelifetech.com, RR : http://fulliengelifetech.com, RR : 311 c 354 g 189 t 8 others
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                                                                                                             Length 1051;
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                                                                                                                              7; Mismatches 17;
                                                                                                             DB 9;
                                                                                                             Score 960.8; DB 9;
Pred. No. 8.5e-127;
                                                                                                           Query Match 46.1%;
Best Local Similarity 97.2%;
Matches 1023; Conservative
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/u.son sapiens"
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/db_xref="taxon:9606"
/clone=lib="txl_Ft015_Brn1"
/sex="manle"
/fissue_type="Adult brain"
/note="vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the NotI and Eco RN sites of the pCMVSPORT 6
vector. Library was constructed by Life Technologies.
Contact: Feng Liang Life Technologies, a division of
Invitrogen 9800 Medical Center Drive Rockville, Maryland
20860, USA Fax: (1) 301 610 8371 Email:
fliang@lifetech.com URL:
http://fulllength.invitrogen.com"
//documents/fulllength.invitrogen.com
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213 TCACCAGCAAACGCCAGGACTTGGBTCCCCCATCCTCAGTACTCACAAGCCATTGCTCCC 154
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BP 191 91006 EVRY cedex - France
Email: segref@genoscope_cns.fr, Web : www.genoscope.cns.fr.
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Mammalia; Euthbaria; Primates; Catarrhini; Hon
Li, Dases 1 to 967)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length CDNA libraries and normalization
Unbublished (2001)
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Pred. No. 1.6e-121;
5; Mismatches 4;
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1. .967
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AL533351.1 GI:12796844
EST.
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ilarity 98.8%;
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167
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AL522712 LILLNFL004_NBC2 Homo sapiens cDNA clone CSODB009YG04 3
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dassa 1 to 978)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Unpublished (2001)

Contact: Genoscope
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Vnote-Torgan: brain, Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 Vector. Library was normalized. Library was constructed by Life Technologies. Contact: From Liang Life Perhologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL: 293 c 331 g 177 t 10 others
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Email: segrefégenoscope.cns.fr, Web : www.genoscope.cns.
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Pred. No. 1.7e-121;
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                                                                                                                                                             /tissue_type="neuroblastoma cells"
/lab_host="DH10B"
                                                              7; Mismatches
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98.6%;
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Li W. B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished (2001)
AACTGAGTGAGGCCCCTGGGTCTGAGGATGGGTCCTGGGGGCCTCGTGTTCATC 1793
                                  1853
                                                                CCCCCATCCTCAGAACTCACAAGCCATTGCTCCCCAGCTGGGGAACCTCAACCTCCCCCC 1913
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BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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Pred. No. 1.1e-118;
1; Mismatches 7; Indels 2
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                       CTATGGGGTCAGCGCCTGTGAGGGCTGCAAGGGCTTCTTCCGGCGCGCAGCATCCAGAAGAA
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AL531149 LT_NFL001_NBC4 H
prime, mRNA sequence.
AL531149 GI:12794642
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BP 191 91006 EVRY cedex - France
Email: segrefégenoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
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1 (bases 1 to 931)
Til,W.B., Gruber,C., Jessee,J. and Polayes,D.
Wull-length CDNA libraries and normalization
Unpublished (2001)
                                         Contact: Genoscope
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 1073)

2 NIH-MGC http://mgc.nci.nih.gov/.

1 National Institutes of Health, Mammalian Gene Collection (MGC)

2 Nothbilshed (1999)

2 Contact: Robert Strausberg, Ph.D.

2 Email: cgapbs-remail.nih.gov

7 issue Procurement: Invitrogen

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library P
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1335 c 302 g 194 t 1 others
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AL551103 993 bp mRNA linear EST 16-FEB-2001 AL551103 LTI_NFL006_PL2 Homo sapiens cDNA clone CSODI066fK12 3

LOCUS

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RESULT 7

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Industrial currents; Catarrhin; Hominidae; Homo.

In (Dases 1 to 993)

In, W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization

Ontact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Colone_lib="LII_NFLO06_PL2"

/tissue_type="powerter" coloned was digested with Not I and enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCANSPORT 6 vector: Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Library publication of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
BP 183 a 291 c 332 g 181 t 6 others
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo
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prime, mRNA sequence.
AL551103
AL551103.1 GI:12888727
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BC030234 3141 bp mRNA linear HTC 20-MAY-2002 Homo saplens, retinoic acid receptor, beta, clone IMAGE:5229160,
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                                                                     678 GAAGGTGCGCAAAGCGCACCAGGAAACCTTCCCTGCCCTCTGCCAGCTGGGCAAATACAC 737
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                                                                                                                                                 GATCCTGCGGATCTGCACGCGGTACACGCCCGAGCAGGACACCATGACCTTCTCGGACGG
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           Length 885;
                                         Indels
Score 729.6; DB 14;
Pred. No. 4.2e-94;
                                       0; Mismatches
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BC030234.1 GI:20988815
HTC.
           35.0%;
91.0%;
         Query Match 35.0
Best Local Similarity 91.0
Matches 785; Conservative
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BC030234
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/organism="Homo sapiens"
/dD_Aref="Laxon:9606"
/clone='Inhage:6282394"
/clone='Inhage:6282394"
/dlone='Inhage:6282394"
/dlone='Inhage:6282394"
/dlone='Inhage:6282394"
/dlone='Inhage:6282394"
/dlone='Inhage:6282394"
/dlone='Organ: spleen; Vector: pOTB7; Site_1: XhOI; Site_2: CoRI; cDNA made by oligo-dr priming. Directionally cloned into EcoRI/XhOI sites using the following 5' adaptor: GGGAGG(G). Library constructed by Ling Homg in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH-MGC Library."

NIH-MGC Library."
337 c 234 g 154 t 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

E (bases 1 to 885)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: Dr. Mark Watson

CONA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM3476 row: 1 column: 11

High quality sequence stop: 599.
                                                                                                                                                                                                                                                                                                                                                                                                                                         AGENCOURT_8351580 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6282394 5', mRNA sequence.
BQ706025
BQ706025
BS706025
EST.
                                                                                                                                                                    GCCTCGTGTTCATCAAGACACCCCTCTGCCCAGCTCACCACATCTTCATCACCAGCAAAC 1839
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                                                                                                                           261 GCCTGGTGTTCATCAAGACACCCTCTGCCCAGCTCACCACATCTTCATCACCAGCAAC
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                                                                                                                                                                        NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs.rfmail.inh.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing Dy: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing Dy: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc.mgc@ehgrinih.gov
Contact: nisc.mgc@ehgrinih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karling,E., Laric,P., Legaspi,R., Maduco,Q.L.,
Masielio,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C., McDowell,J.,
Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W., Tsurgeon,C.,
Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A.,
Zhang,L.-H. and Green,E.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                be found
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 14916493
This clone has the following problem: frame shifted.

Location/Qualifiers
                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3141)
                                                                                           Direct Submission
Submitted (07-MAY-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   662
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663 c 633 g 859 t
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/organism="Homo sapiens"
/db_xref="LocusID:5915"
/db_xref="taxon:9606"
/clone="IMAGE:5229160"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="Pancreas, 8/clone_lib="NIH_MGC_120"
/lab_host="DH10B"
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Matches 836; Conservative
                                                                              Strausberg, R
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               ORGANISM
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BI827961 702 bp mRNA linear EST 04-OCT-2001 603073894F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5165734 .5',
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NIH-WGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                  1023 CGACTGGACCTCTGGGACAAATTCAGTGAACTGGCCACCAAGTGCATTATTAAG 1082
                                                                                                                                                                                                                                                                                                                                                                                                    1203 CCAGAACAAGACACCATGCTCAGACGCCTTACCCTAAATCGAACTCAGATGCAC 1262
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705
                                                                                                 903 GAAATGACAGCTGAGTTGGACGATCTCACAGAGAAGATCCGAAAAAGTTCGAAGAAACT 962
                                                                                                                                                                     706 TICCCIGCCCTCTGCCAGCTGGGCAAATACACTACGAACAACAGCTCAGAACAACGTGTC 765
                                                                                                                                                                                                                                                                         766 TCTCTGGACATTGACCTCTGGGACAAGTTCAGTGAACTCTCCACCAAGTGCATCATTAAG 825
                                                                      646 ACGCTGACGCCGGAGGTGGGGGAGCTCATTGAGAAGGTGCGCAAAGCGCACCAGGAAACC
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Query Match 31.4
Best Local Similarity 100.
Matches 654; Conservative
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KEYWORDS
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;
                             Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.l column: 23
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Pred. No. 3.6e-84;
0; Mismatches 12; Indels 2;
                                                                                                                                                                                                                                                                                      /clone_lib="NIH_MGC_119"
/tissue_type="medulla"
/lab_host="DH10B"
                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5165734"
                 Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                     High quality sequence stop: 622.
Location/Qualifiers
1. .702
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98.0%;
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/clone_Inb="NoT.GAP.Carl"
/clone_Inb="NoT.GAP.Carl"
/tissue_type="Osteoarthritic Cartilage"
/dev_stage="Adult"
/lab_host="Adult"
/lab_host="DH10B [Life Technologies]"
/note="Organ: Rnee; Vector: pT7T3-Pac (Pharmacia) with a modified Polylinker; Site_1: EcoR I; Site_2: Not I;
NCI_CGAP_Carl is a cDNA library containing the following tissue(s): Osteoarthritic Cartilage The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector: The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov The following repetitive elements were found in this CDNA sequence: 1-73, >AT_rich#Low_complexity (matched compliment) POLYA-Yes.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                           BQ044936 tinear EST 28-MAR-2
UI-H-EUO-azo-e-05-0-UI.s1 NCI_CGAP_Carl Homo sapiens cDNA clone
IMAGE:5851372 3', mRNA sequence.
GGGGTGGGGGGGGGGGGGGGGCTGCCCCCCCCCCCCAGGCAGCT-GTAGCCCCAGC
                                                                                                                                                              Length 654;
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TAG_SEQ=TGATCACGCT"
161 c 227 g 131 t
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100.0%; Pred. No. 2.5e-83;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
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/clone="IMAGE:5851372"
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Unpublished (1997)
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/clone="INAGES:5768263"
/clone="INAGES:5768263"
/clone="INAGES:5768263"
/clone="INAGE_11b="NnH_MGC_121"
/lab_host="Dist="NnH_MGC_121"
/note="Organ: brain; Vector: pcMV-SPORT6; Site_1: NotI;
Site_2: EccRV (destroyed); RNA Source anonymous pool of 3
Site_2: EccRV (destroyed); RNA Source anonymous pool of 3
fetal brains, female age 20 weeks, female age 24 weeks,
and male age 26 weeks. Library is oligo-dT primed and
directionally cloned (EccRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
0.7-3.5 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Innitrogen). Research Genetics tracking code 017. Note:
this is a NIH MGC Library.
8 a 339 c 286 g 188 t
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Pred. No. 1.1e-82;
0; Mismatches 11
                                                /db_xref="taxon:9606"
Location/Qualifiers
                              /organism="Homo
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Best Local Similarity 98.3%;
Matches 655; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1091)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
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Email: cgapbs-rémail.nih.gov
Tissue Procurement: Life Technologies, Inc.
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lln.gov
Plate: LLAM12827 row: n column: 08
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VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

JOURNAL TITLE COMMENT

DEFINITION

ACCESSION

RESULT 12 BM927280

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                              EST 18-DEC-1999
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                                                                                                                                                      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 703)
NCI-CGAP http://www.nobi.nlm.nih.gov/ncicgap.
NAI-CGAP http://www.nobi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                  Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs r@mail.nih.gov
Inis clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 794 Std Error: 0.00.
Seg primer: -40UP from Gibco
High quality sequence stop: 469.
Location/Qualifiers
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A1806984.1 G1:5393550
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Pred. No. 3.8e-82;
0; Mismatches 23; Indels
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/db_xref="taxon:9506"
/clone="InAGE:2356574"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH108"
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Best Local Similarity 96.5%;
Matches 680; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthoria; Primates; Catarrhini; Hominidae; Homo.

E. (bases 1 to 1164)

National Institutes of Health, Mammalian Gene Collection (MGC)

L. Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM10079 row: O column: 23

High quality sequence stop: 677.
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/db_xref="taxon:9606"
/clone="INAGE:4396510"
/clone=lib="NIH_MACE:84396510"
/clone_lib="NIH_MACE:86"
/tissue_type="Osteosarcoma, cell line"
/tissue_t
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Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                        121 AGCCTCAGCCCCAGCTCCAACAGAAGCAGCCGGCCACCCCACTCCCCGTGACCGCCCACG
                                                                                                                                                                                                TGACCCCGCACCAGCCCTGCCCCCACCTGCCGGGCAGTACTGGGGACCTTCCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Korea Research Institute of Bioscience & Biotechnology 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea Tel: +82-42-860-4470
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JOURNAL
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/note="Organ: Stomach; Vector: pT218RP1; Site_1: ECORI; Site_2: Not1; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR is site by treatment of T4 RNA ligase and the first strand CDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The CDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by GASyamma Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli ToplOF' by electroporation method. The cDNA libraries constructed by this method are full-length enriched CDNA library."
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Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
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Location/Qualifiers
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                                       GENERAL INFORMATION:

APPLICANT: Calabretta, Bruno
APPLICANT: Calabretta, Bruno
APPLICANT: Skorski, Tomasz
TITLEOF INVENTION: ANTISENSE
TITLE OF INVENTION: ANTISENSE
TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, P.C.
STREET: Two.Penn Center, Suite 1800
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19102
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                                                                                                                                                                                                                                                                                                                                                                    COMPUTER FEADBLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
COMPUTER: TBM PS/82
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/306,691B
FILING DATE: September 15, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
FILING DATE:
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99.8%; Pred. No. 0;
11ve 0; Mismatches
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REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 3821-8
TELECOMMUNICATION INFORMATION:
TELEPAX: (215) 568-5549
TELEFAX: (215) 568-5549
ITELEX: No. 5734039e
INFORMATION FOR SEQ ID NO: 52:
Sequence 52, Application US/08306691B Patent No. 5734039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
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LENGTH: 3036 base pairs
TYPE: nucleic acid
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Best Local Similarity 99.8
Matches 1784; Conservative
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Sequence

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	350 CTCTACCCCGCATCTACAAGCCTTGCTTTGTCTGTCAGGACAAGTCCTCAGGCTACCACT 409 	410 1370	470 TGGTGTACACGTGTCACCGGACAAGAACTGCATCATCAACAAGGTGACCGGAACCCCT		590 ACGACCGAAACAAGAAGAAGAAGGGGCCCCAAGCCCGAGTGCTCGGGAGCTACACGC 649 	650 TGACGCCGGAGGTGGGGAGCTCATTGAGAAGGTGCGCAAAGCGCACCAGGAAACCTTCC 709 	710 CTGCCCTCTGCCAGCTGGGCAAATACACTACGAACAACAGCTCAGAACAACGTGTCTCC 769 	770 TGGACATTGACCTCTGGGACAAGTTCAGTGAACTCTCCACCAAGTGCATCATTAAGACTG 829 	830 TGGAGTTCGCCAAGCAGCTGCCCGGCTTCACCACCTCACCATCGCCGACCAGATCACCC 889	890 TCCTCAAGGCTGCCTGCCTGGACATCCTGGGGATCTGCAGGGGTACAGGCCG 949 	950 AGCAGGACACCATGACCTTCTCGGACGGCCTGAACCGGACCGAGATGCACAGAGG 1009 	1010 CTGGCTTCGGCCCCTCACCGACTGGTCTTTGCCTTCGCCAACCAGCTGCTGCCCTGG 1069	1070 AGATGGATGATGCGGAGACGGGGCTGCTCAGCGCCATCTGCCTCATCTGCGGAGACCGCC 1129 	1130 AGGACCTGGAGCGGACCGGGTGGACATGCTGCAGAGCCGCTGCTGGAGGCGCTAA 1189 	1190 AGGTCTACGTGCGGAAGCGGAGGCCCAGCCCCCCACATGTTCCCCAAGATGCTAATGA 1249 	1250 AGATTACTGACCTGCGAAGCATCAGCGCCAAGGGGCTGAGCGGGTGATCACGCTGAAGA 1309 	1310 TGGAGATCCCGGGCTCCATGCCGCCTCTCATCCAGGAAATGTTGGAGAACTCAGAGGGCC 1369 11111111111111111111111111111111111	1370 TGGACACTCTGAGCGGACAGCCGGGGGGGGGGGGGGGGG
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FILING DATE: 21-JUL-1993
CLASSIFTCATION: 435
PRIOR APPLICATION 1435
APPLICATION DATE: 20.000
FILING DATE: 22-MAR-1991
ATTORNEY AGENT INFORMATION:
NAME: WHITE, JOHN P
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 38694-A
TELECHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3036 base pairs
TYPE: nucleic acid
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99.8%;
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OTHER INFORMATION:
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US-08-095-728B-1
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                                                                           Sequence 1, Application PC/TUS9202320A
GENERAL INFORMATION:
APPLICANT: Sloan-Kettering Institute, For Cancer Research
TITLE OF INVENTION: METHODS FOR DETECTION AND TREATMENT OF CORRESPONDENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & DINHAM
STREET: 30 ROCKEFELLER PLAZA
              2990 TIGITITGATTITTTAATAAGAATTITGATTTAAGGAAAAAA 3036
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2030 IIGITITGATITITITAATAAGAATTTTCATTTTAAGCACAAAAAA
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0; Mismatches
                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US92/02320A
                                                                                                                                                                                                                                                                                                                                                                                                                         28,678
ER: 38694-PCT
                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 675,084
FILING DATE: 22-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 673,838
FILING DATE: 22-MAR-1991
ATTORNEY AGENT INFORMATION:
NAME: WHITE, JOHN P
REGISTRATION NUMBER: 38,678
REFERENCE/DOCKET NUMBER: 38,694-PC
TELECOMMUNICATION INFORMATION:
TELEFAN: (212) 677-9550
TELEFAN: (212) 44-0555
TELEFAN: (212) 44-0555
TELEFAN: (212) 42253 COOP UI
                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 3036 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 99.8
Matches 1784; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67..2457
                                                                                                                                                                                                                                                COMPUTER: IBM PC OPERATING SYSTEM: SOFTWARE: Patenti
                                                                                                                                                 ADDRESSEE: COOPER
STREET: 30 ROCKEF
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: CDNA IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLONE: MYL-RAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
                                                        RESULT 3 '
PCT-US92-02320A-1
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                                                                                           1490 GCCAGTACTGCCGACTGCAGAAGTGCTTTGAAGTGGGCATGTCCAAGGAGTCTGTGAGAA
                                                                                                                                                                         650 TGACGCCGGAGGTGGGGGAGCTCATTGAGAAGGTGCGCAAAGCGCACCAGGAAACCTTCC
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                                                                         GCCAGTACTGCCGACTGCAGAAGTGCTTTGAAGTGGGGCATGTCCAAGGAGTCTGTGAGAA
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TGGTGTACACGTGTCACCGGGACAAGAACTGCATCAACAAGGTGACCCGGAACCCCT
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1010 CTGGCTTCGGCCCCCTCACCGACCTGGTCTTTGCCTTCGCCAACCAGCTGCTGCCCCTGG 1069
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                                                              2630 GCCTGGGCCCTCAGTGGACTGCCTGCTCCACAGCCTGGGCTGACGTCAGAGGCCGAGGC 2689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 13, Application US/08892747

Fatent No. 6057153

GENERAL INFORMATION:

APPLICANT: Shall T. George, Michael Ma, Martina Werner,

APPLICANT: Shall T. George, Michael Ma, Martina Werner,

TITLE OF INVENTION:

APPLICANT: Underto Pace and Allan R. Goldberg

TITLE OF INVENTION:

APPLICANT: Underto Pace and Allan R. Goldberg

TITLE OF INVENTION:

APPLICANT: Underto Pace and Allan R. Goldberg

APPLICANT: 2800 Underto Steert

APPLICANT: 2800 Underto Allante

STREET: 1201 West Peachtree Street

COUNTR: USA

ALLanta

COUNTR: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: TIBM PC Compatible

COMPUTER: IBM PC Compatible

COMPUTER: IBM PC Compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: January 13, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/00513
FILING DATE: January 19, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/892,747 FILING DATE:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/372,556
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US-08-892-747-13
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                                                                                                                                                                                                                                                                                                                                                                            85.4%; Score 1782.2; 99.8%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: ILLIT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 3511 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature LOCATION: 1..3511
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HYPOTHETICAL: NC
ANTI-SENSE: NO
FEATURE:
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APPLICANT: DMITROSKY, ETHAN
APPLICANT: WARRELL JR, RAYMOND P
APPLICANT: WALLES JR, WILSON H
APPLICANT: FRANKEL, STANDEN
TITLE OF INVENTION: METHODS FOR THE DETECTION AND
TITLE OF INVENTION: TREATMENT OF ACUTE PROMYELOCYTIC LEUKEMIA (APL)
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & DUNHAM LLP
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Best Local Similarity 99.3%; Pred. No. 0;
Matches 1786; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/095,728B
FILING DATE: 21-JuL-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/673,838
FILING DATE: 22-MAR-1991
ATTORNEY APPLICATION NUMBER: US 07/673,838
FILING DATE: 22-MAR-1991
ATTORNEY AGENT INFORMATION:
NAME: WHITE, JOHN P
REGISTRATION NUMBER: 28,678
REFREENCE/DOCKET NUMBER: 38694-A
FELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEPONE: (212) 391-0525
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                              E: COOPER & DUNHAM LLP
1185 AVENUE OF THE AMERICAS
Sequence 3, Application US/08095728B Patent No. 5843642
                                                                                                                                                                                                                                                                   CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
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CTHER INFORMATION:
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                                       GENERAL INFORMATION
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		AAACGACCGAAACAAGAAGAAGAAGGTGCCCAAGCCCGAGTGCTCTGAGAGTTACAC 	GCTGACGCCGGAGGTGGGGGAGCTCATTGAGAAGGTGCGCAAAGGGCACCAGGAAACCTT 	CCCTGCCCTCTGCCAGCTGGGCAAATACACTACGAACAACAGCTCAGAACAACGTGTCTC	TCTGGACATTGACCTCTGGGACAAGTTCAGTGAACTCTCCACCAAGTGCATCATTAAGAC	TGTGGAGTTCGCCAAGCAGCTGCCCGGCTTCACCACCCTCACCATCGCCGACCAGATCAC	CCTCCTCAAGGCTGCCTGCACATCCTGATCCTGCGGATCTGCACGCGGTACACGCCC	CGAGCAGGACCATGACCTTCTCGGACGGGCTGACCCTGAACCGGACCCGATGCACAA 	CGCTGGCTTCGGCCCCTCACCGACCTGGTCTTTGCCTTCGCCAACCAGTGCTGCCCCT	GCAGATGCTCATCTGCGCAGACGGGGCTGCTCAGCGCCATCTGCCTCATCTGCGAGACCG	CCAGGACCTGGAGCCGGACCGGGTGGACATGCTGCAGGAGCCGCTGCTGGAGGCGCTT	AAAGGTCTACGTGCGGAAGCGGAGGCCCAGCCCCCCACATGTTCCCCAAGATGCTAAT 	GAAGATTACTGACCTGCGAAGCATCAGCGCCAAGGGGGCTGAGGGGGGGG	GATGGAGATCCCGGGCTCCATGCCGCCTCTCATCCAGGAAATGTTGGAGAACTCAGAGGG 	CCTGGACACTCTGAGCGGACACCCGGGGGGGGGGGGGGG	CCCGCCAGGCAGCTGTAGCCCCAGCCTCAGCCCCAGCTCCAACAGAAGCAGCCCGGCCAC	CCACTCCCCGTGACCGCCCACGCCACATGGACACAGCCCTCGCCCTCGGCCCGGGCTTTT	CTCTGCCTTTCTACCGACCATGTGACCCCGCACCAGCCCTGCCCCACCTGCCCTCCCGG	GCAGTACTGGGGACCTTCCCTGGGGGACGGGGGGGGGGG

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METHODS FOR DETECTION AND TREATMENT OF CANCER
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PCT/US92/02320A
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UMBER: 38694-PCT
SCRMATION:
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Pred. No. 0;
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LOCATION:
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                                 GAAGATTACTGACCTGCGAAGCATCAGCGCCCAAGGGGGCCTGAGCGGGTGATCACGCTGAA
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Patent No. 5830760
GENERAL INFORMATION:
APPLICANT: TSai, S. and S.J. Colling TITLE OF INVENTION: "Hematopoletic NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
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STREET: 28
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                                                                                                                                                                                                                                                                                              Length 2940;
                                                                                                                                                         TELEPHONE: 1-206-682-8100; 1-206-224-0709(direct)
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2940 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                            DB 2;
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                     ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKette-5.25 inch, 1.2Mb stc
COMPUTER: IBM PC/386 Compatible
OPERATING SYSTEM: MS-DOS 4.01
SOFTWARE: WORD FOR WINDOWS 5.01-t
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,383
                                                                                                                                                                                                                                                          Score 1777.2;
Pred. No. 0;
0; Mismatches
                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/099,242
FILING DATE: JULY 28, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Broderick, Thomas F.
REGISTATION NUMBER: 31,332
REFERENCE/DOCKET NUMBER: FHCR-1-7190
TELECOMMUNICATION:
                                                                                                                                                                                                             MOLECULE TYPE: CDNA to MRNA
DESCRIPTION: see Figure 16B; RAR-alpha
IMMEDIATE SOURCE:
                                                                f DATA:
                                                                                                                                                                                                                                                          85.2%;
99.3%;
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Matches 1785; Conservative
         Washington
                USA
                                                                                  FILING DATE:
CITY: Se
STATE: W
COUNTRY:
                                                                                                                                                                                                                                     LIBRARY:
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US-08-592-383-1
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           GGAGATGGATGCGGGGGGGGGCTGCTCAGCGCCCATCTGCCTCATCTGCGGAGACCG
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                                                                                                                 C.; UEMSONO, KAZUHIKO
                                                                                                                                                                                                                           DB
                                                                                                                          NUMBER OF SEQUENCES: 2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 05.07/546,256
FILING DATE: 06-NUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 276,536
FILING DATE: 30-NOV-1988
APPLICATION NUMBER: 128,331
FILING DATE: 02-DEC-1987
                                                                                                                                                                                                                          Score 1777.2;
Pred. No. 0;
0; Mismatches
                                                                                         S171671-1

; Patent No. 5171671

; Patent No. 5171671

; PRUDIMAR S.; THOMPSON, CATHERINE C.; UEMSC, GUGUERE, VINCENT

; TITLE OF INVENTION: RETINOIC ACID RI

NUMBER OF SEQUENCES: 2

; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/546,25:

; FILING DATE: 06-AUG-1990

; ROOM REPLICATION DATA:

APPLICATION NUMBER: 276,536

; RILING DATE: 30-NOV-1988
                                                                                                                                                                                                                         Query Match 85.2%;
Best Local Similarity 99.3%;
Matches 1785; Conservative
                                                                                                                                                                                                     LENGTH: 2940
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1007 1067 1058 1127 1187 1178 1247 1238 1307 1367 1358 1427 1418 1478 1487 1547 1538 1667 1607 1598 1658 1727 1787 1907 966 878 947 938 887 GGAGATGGATCATGCGGAGACGGGGTGCTCAGCGCCATCTGCCTCATCTGCGGAGACCG CGAGCAGGACACCATGACCTTCTCGGACGGGCTGACCCTGAACCGGACCCAGATGCACAA CCTCCTCAAGGCTGCCTGCCTGGACATCCTGATCTGCGGATCTGCACGCGGTACACGCC GAAGATTACTGACCTGCGAAGCATCAGCGCCAAGGGGGCTGAGCGGGTGATCACGCTGAA CCCGCCAGGCAGCTGTAGCCCCAGCCTCAGCCCCAGCTCCAACAGAAGCAGCCCGGCCAC CTCTGCCTTTCTACCGACCATGTGACCCGCACCAGCCCTGCCCCCACCTGCCCTCCCGG GATGGAGATCCCGGGCTCCATGCCGCCTCTCATCCAGGAAATGTTGGAGAACTCAGAGGG AGGCCTGGGCCCTCAGTGGACTGCCTCCCACAGCCTGGGCTGACGTCAGAGGCCGAG GCCAGGAACTGAGTGAGGCCCCTGGTCCTGGGTCTCAGGATGGGTCCTGGGGGCCTCGTG TTCATCAAGACACCCCTCTGCCCAGCTCACCACTTCTTCATCACCAGGAACGCCAGGAC TTGGCTCCCCCATCCTCAGAACTCACAAGCCATTGCTCCCCAGCTGGGGAACCTCAACCT us-09-691-220-1.rni

QY 468 CATGGTGTACACGTGTCACCGGGACAAGAACTGCATCATCAACAAGGTGACCCGGAACCC 527 DD 459 CATGGTGTACACGGGACAAGAACTGCATCATCAACAAGAGTGACCCGGAACCG 518 QY 528 CTGCCAGTACTGCAGAAGTGCTTTGAAGTGGGCATGTCCAAGGAGTCTGTGAG 587 DD 519 CTGCCAGTACTGCAGAAGTGCTTTGAAGTGGGCATGTCCAAGGAGTCTGTGAG 578 QY 588 AAACGACCGAAACAAGAAGAAGAAGAAGGAGGTGCCCAAGCCCGAGTGCTCTGAAGGTAACTAAC	648 GCTGACGCGGGGGGGGGGCTCATTGAGAAGGTGCGCAAAGCGCACCAGGAAACCTT 70 11111111111111111111111111111111111	928 TGTGGAGTTCGCCAAGCTGCCCGGCTTCACCACCTCACCATCGCCGACCAGATCAC 887	DD 939 CCAGCAGGACACCATGACCTTCTGGACGGCTGACCCTGAACCGGACCCAGATGCACAA 998	QY 1128 CCAGGACCTGGAGCAGCCGGACGGACATGCTGCAGGAGCCGCTGCTGGAGGCGCT 1187 D 1119 CCAGGACCTGGAGCCGGACCGGGTGGACATGCTGCAGGAGCCGCTGCTGGAGGCGCT 1178 QY 1188 AAAGGTCTACGTGCGGAGCCCAGCCGCCCCCCCACATGTTCCCCAAGATGCTAAT 1247 D 1179 AAAGGTCTACGTGCGAAGCGGAGCCCAGCCGCCCCCCACATGTTCCCCAAGATGCTAAT 1247 D 1179 AAAGGTCTACGTGCGAAGCGGAGCCCAGCCGCCCCCACATGTTCCCCAAGATGCTAAT 1238 QY 1248 GAAGATTACTGACCTGCGAAGCATCAGCGCCCAAGGGGGCTGAGGTGATCACGCTGAA 1307 D 1239 GAAGATTACTGACCTGCGAAGCATCAGCGCCCAAGGGGGCTGAGCGGTGATCACGCTGAA 1298 D 1239 GAAGATTACTGACCTGCGAAGCATCAGCGCCCAAGGGGGCTGAGGGTGATCACGCTGAA 1298	QY 130B GATGGAGATCCCGGGCTCCATGCCGCCTCTCATCCAGGAAATGTTGGAGAACTCAGAGGG 1367 Db 1299 GATGGAGATCCTAG QY 136B CCTGGACACTCTGAGCGGGGGGGGGGGGGGGGGGGGGGG
Db 1899 CCCCCCTGCTCGGTTGGTGAGGGGGTGGGACAGGGGGGGG	RESULT 9 US-08-592-383-3 ; Sequence 3, Application US/08592383 ; Patent No. 5830760 ; GENERAL INFORMATION: ; APPLICANT: TIAI, S. and S.J. Collins ; TITLE OF INVENTION: "Hematopoietic Cell Lines Bearing Altered Retinoic Acid Recept ; NUMBER OF SEQUENCES: 10 ; CORRESPONDENCE ADDRESS: ; ADDRESSE: Christensen, O'Connor, Johnson and Kindness ; STREET: 2800 Pacific First Centre, 1420 Fifth Avenue	CITY: Seattle STATE: Washington COUNTRY: USA 2 IP: 98101 COMPUTER READABLE FORM: MEDIOM TYPE: Diskette-5.25 inch, 1.2Mb storage COMPUTER: IBM PC/386 Compatible OPERATING SYSTEM: MS-DOS 4.01 SOFTWARRE: Word for Windows 5.01-t CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/592,383	FILING DATE: CLASSIFICATION: 435 FROR APPLICATION DATA: APPLICATION NUMBER: 08/099,242 FILING DATE: July 28, 1993 ATTORNEY/AGENT INFORMATION: NAME: Broderick, Thomas F. REGISTRATION NUMBER: 31,332 FEFERENCE/DOCKET NUMBER: FHCR-1-7190	TELECHMONICATION INFORMATION: TELECHNONE: 1-206-682-8100; 1-206-224-0709(direct) TELEPHONE: 1-206-682-8100; 1-206-224-0709(direct) SEQUENCE CHARACTERISTICS: LENGTH: 2658 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear MOLECULE TYPE: cDNA to mRNA DESCRIPTION: page 4, RAR-alpha403 dominant negative; deleted of 1311-1596 of SEQ. IMMEDIATE SOURCE: LIBRARY: cDNA	Ouery Match Query Match Best Local Similarity 83.5%; Score 1200; DB 2; Length 2658; Best Local Similarity 83.5%; Pred. No. 1.2e-233; Matches 1501. Qy 288 CTCCATTGAGGCCCGGGCGTTCTGAGGATTGTCCCCCCCC

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PAPLICANT: TAKAKU, FUMIMARO; ISHIKAWA, TAKASHI; IMAWARI, MICHIO; FVANS, RONALD M.; UMESONO, KAZUHIKO

TITLE OF INVENTION: HUMAN GAMMA RETINOIC ACID RECEPTOR DNA NUMBER OF SEQUENCES: 4

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/370,407

FILING DATE: 22-UUN-1989
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Best Local S:
Matches 883,
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Bearing Altered Retinoic Acid Rec
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                                                                                                    AACGACCGAAACAAGAAGAAGAAGGAGGTGCCCAAGCCCGAGTGCTCTGAGAGCTACACG
            CCTGCCCTCTGCCAGCTGGGCAAATACACTACGAACAACAGCTCAGAACAACGTGTCTCT
                                                                                                                                      CTGGACATTGACCTCTGGGACAAGTTCAGTGAACTCTCCACCAAGTGCATCATTAAGACT
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1420 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/08592383
Patent No. 5830760
GENERAL INFORMATION:
APPLICANT: TSA1, S. and S.J. Collins
TITLE OF INVENTION: "Hematopoietic Cell Lines is CORRESSPONDENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Christensen, O'Connor, Johnson and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 2800 Pacific First Centre,
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STATE: Washington
COUNTRY: USA
ZIP: 98101
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                              534 CTTCCTCCCCCTCGAGTGTACAAACCCTGCTTCGTCTGCCAGGACAAATCATCAGGGTAC
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                                                                                                                                                              Patent No. 5223606

Patent No. 5223606

Patent No. 5224606

Patent No. 5224606

PIERRE; DELAMIN DE THE, HUGHES; MARCHIO, AGNES; TIOLLAIS, TIERE; DELAMIN AND STEROID/THYROID HORMONE RECEPTOR-RELATED

PROTEIN INAPPROPRIATELY EXPRESSED IN HUMAN HEPATOCELLULAR CARCINOMA
                                                                                                                                                                                                                                                                                                                                                          Length
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                                                                       CAGAGGGCCTGGACACTCTGAGCGGACAGCCGGGGGGGTGGGGGGG
                                                                                                                                                                                                                                                                                                                                                          Score 667.8; DB 6;
Pred. No. 4e-126;
); Mismatches 262;
                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 11
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/134,130
FILING DATE: 17-DEC-1987
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                             32.0%;
76.1%;
                                                                                                                                                                                                                                                                                                                                                             Query Match 32.0
Best Local Similarity 76.1
Matches 836; Conservative
                                                                                                                                                                                                                                                                                                                    LENGTH: 2989
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                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: CDNA to mRNA
DESCRIPTION: page 11; RAR-alpha RA binding region; positions 692 to 1395 of SEQ.
IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                    Length 704;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 1-206-682-8100; 1-206-224-0709(direct)
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette-5.25 inch, 1.2Mb storage COMPUTER: IBM FO/386 COMPAtible OPERATING SYSTEM: MS-DOS 4.01
SOFTWARE: Word for Windows 5.01-t
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 702.4; DB 2;
Pred. No. 2.7e-133;
0; Mismatches 1;
                                                                                                                                                                                                          FHCR-1-7190
                                                                                  US/08/592,383
                                                                                                                                        08/099,242
                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/099,24
FILING DATE: July 28, 1993
ATORNEY/AGENT INFORMATION:
NAME: Broderick, Thomas F.
REGISTRATION NUMBER: 31,332
REFERENCE/DOCKET NUMBER: FHCR
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 33.7%;
Best Local Similarity 99.9%;
Matches 703; Conservative
                                                                                                                                                                                                                                                                          LENGTH: 704 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                        DATA:
                                                                   CURRENT APPLICATION DAY
                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                              CDNA
                                                                                                FILING DATE
                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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US-08-592-383-5
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                                                                                                                                                     1254 TITGGAAATGGATGACACAGAAACAGGCCTTCTCAGTGCCATCTGCTTAATCTGTGGAGA 1313
                                                                                                                                                                                                                                                                        1065 CCTGGAGATGGATGATGCGGAGACGGGGCTGCTCAGCGCCATCTGCCTCATCTGCGGAGA 1124
                                                                                                                                                                                                     AATGAAGATTACTGACCTGCGAAGCATCAGCGCCCAAGGGGGCTGAGCGGGTGATCACGCT 1304
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              1194 CAATGCTGGATTTGGTCCTCTGACTGACCTTGTGTTCACCTTTGCCAACCAGCTCCTGCC
                                                                                                                                                                                    CCGCCAGGACCTGGAGCAGCCGGACCGGGTGGACATGCTGCAGGAGCCGCTGCTGGAGGC
                                                            1005 CAACGCTGGCTTCGGCCCCCTCACCGACCTGGTCTTTGCCTTCGCCAACCAGCTGCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Rothschild, Max F.
APPLICANT: Tuggle, Chrisopher K.
APPLICANT: Messer, Lori A.
APPLICANT: Messer, Lori A.
APPLICANT: Tun-Ping, Yu APPLICANT: Tun-Ping, Yu APPLICANT: Tun-Ping, Tun TITLE OF INVENTION: GENES AND GENETIC MARKERS FOR IMPLITIE OF INVENTION: REPRODUCTIVE TRAITS IN ANIMALS NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zarley, McKee, Thomte, Voorhees & Sease STREET: 801 Grand Avenue, Suite 3200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSEE: Zarley, McKee, Thomte, Voorhees & Sease
1: 801 Grand Avenue, Suite 3200
Des Moines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ISURF 021591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/896,365
FLING DATE: 18-UL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/022,180
FILING DATE: 19-UL-1996
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/08896365
Patent No. 5939264
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37,719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 515-288-3667
TELEFAX: 515-288-1338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1554 AGGACATGAACCCTTGACC 1572
                                                                                                                                                                                                                                                                                                                                                                                                                                          1365 GGCCTGGACACTCTGAGC 1383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Nebel, Heidi S. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 50309
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Iowa
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Sequence 6, Application US/08592383
Patent No. 5830760
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: "Hematopoietic Cell Lines Bearing Altered Retinoic Acid Rec NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
STREET: 2800 Pacific First Centre, 1420 Fifth Avenue
                                                                                                                                                                                                                                                                                                      ;
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1123 GACCGCCAGGACCTGGAGCCGGACCGGGTGGACATGCTGCAGGAGCCGCTGCTGGAG 1182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1064 CCCTGGAGATGGATGCGGAGACGGGGCTGCTCAG-CGCCATCTGCCTCATCTGCGGA 1122
                                                                                                                                                                                                                                                                                                                                                                                                                                   649 CTGACGCCGGAGGTGGGGGAGCTCATTGAGAAGGTGCGCAAAGCGCACCAGGAAAC-CTT 707
                                                                                                                                                                                                                                                                                                                                                                                                               708 CCCTGCCCTCTGCCAGCTGGGCAAATACACTACGAACAACAGCTCAGAACAACGTGTCTC 767
                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      886 ACCTCCTCAAGGCTGCCTGCCTGGACATCCTGATCCTGCGGATCTGCACGCGGTACACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGTGGAGTTCGCCAAGCAGCTGCCCGGCTTCACCACCCT-CACCATCGCCGACCAGATC
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                                                                                                                                                                                                                                                                Length 558;
                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                     Ouery Match 14.1%; Score 293.4; DB 2; Best Local Similarity 77.2%; Pred. No. 1e-50; Matches 429; Conservative 0; Mismatches 121;
                                                     TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
MATT: SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Porcine embryo RARG
DEVELOPMENTAL STRGE: Embryo
US-08-896-165-5
: 558 base pairs
nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1183 GCGCTAAAGGTCTACG 1198
                    TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                543 GCCTGAGGCTCTATG
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STATE: Washington
COUNTRY: USA
  LENGTH:
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779 ACCICIGGGACAAGIICAGIGAACICICCACCAAGIGCAICATIAAGACIGIGGAGIICG 838
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       863 ACCCTGTCACCAACATTGCCCAAGCAGCCGACAAACAGCTTTTCACCCTGGTGGAGTGGG 922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -GCAGCGTGGCAAGGACCGGAAGAATGAGGTGGAGTCGACCACCAGCACCAACGAGG 760
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 183; DB 1; Length 186
Pred. No. 3e-28;
0; Mismatches 500; Indels
Patentin Release #1.0, Version #1.25
                                                     APPLICATION NOMBER:

CLASSIFICATION: 435
PRIOR APPLICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/933,453
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US91/00399
FILING DATE: 22-JAN 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/478,071
FILING DATE: 09-FEB-1990
ATTONREY/AGENT INFORMATION:
NAME: REITER, STEPHEN E.
REGISTRATION NUMBER: 31,192
REGISTRATION NUMBER: 31,192
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                821 ACGTGGAGGCAAACATGGGGCTGAACCCCCAGCTC--
                          UMBER: US/08/336,408B
08-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 50.6%;
Matches 537; Conservative
                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 619-546-9392
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1866 base palrs
                      CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ), NAME/KEY: CDS
; LOCATION: 76..1464
US-08-336-408B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: both
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   both
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            433 TGCAAGGGCTTCTTCCGCCGCAGCATCCAGAAGAACATGGTGTACACGTGTCACCGGGAC 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAGAACTGCATCATCAACAAGGTGACCCGGAACCCTGCCAGTACTGCCGACTGCAGAAG 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 201;
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Patent No. 572329
GENERAL INFORMATION
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: MANGELSDORF, DAVID J.
TITLE OF INVENTION: RETINDID RECEPTOR COMPOSITIONS AND TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK STREET: 444 SOUTH FLOWER STREET, SUITE 2000 CITY: LOS ANGELES STATE: CA
                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 1-206-682-8100; 1-206-224-0709(direct)
FORMATION FOR SEQ ID NO: 6:
                                      MEDIUM TYPE: Diskette-5.25 inch, 1.2Mb storage COMPUTER: IBM PC/386 Compatible OPERATING SYSTEM: MS-DOS 4.01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.6%; Score 199.4; DB 2;
99.5%; Pred. No. 7.5e-32;
tive 0; Mismatches 1;
                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PILING DATE: 08/099,242
FILING DATE: July 28, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Broderick, Thomas F.
REFERENCE/DOCKET NUMBER: 31,332
REFERENCE/DOCKET NUMBER: FHCR-1-7190
                                                                                               SOFTWARE: Word for Windows 5.01-t
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGCTTTGAAGTGGGCATGTCC 573
                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 201 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity 99.5'
Matches 200; Conservative
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                          COMPUTER READABLE FORM:
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                                                                                                                                                                 FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIBRARY:
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959 CCATGACCTTCTCGGACGGGCTGACCCGAACCCAGATGCACACGCTGGCTTCG 1018
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                                                                                                                                                                                                                                         1043 GGATCCTCCTGGCCACCGGGCTGCACGTCCACCGGAACAGCGCCCACAGAGCGCAGGGGTGG 1102
                                                                                                                                                   1136 TGGAGCAGCCGGACCGGGTGGACATGCTGCAGGAGCCGCTGCTGGAGGCGCGTAAAGGTCT 1195
                                                                                                                                                                                                                                                                      1196 ACGTGCGGAAGCGGAGGCCCAGCCCCCACATGTTCCCCAAGATGCTAATGAAGATTA 1255
                                                                                                                                                                                                                                                                                                                   1256 CTGACCTGCGAAGCATCAGCGCCCAAGGGGGCTGAGCGGGTGATCACGCTGAAGATGGAGA 1315
                                                                                                                                                                                                                                                                                                                                  899 CIGCCIGCACAICCIGAICCIGCGGAICIGCACGCGGIACACGCCGGAGCAGGACA 958
                                                                                                                                                                                                                                                                                                                                                               1316 TCCCGGGCTCCATGCCGCCTCTCATCCAGGAAATGTTGGAG 1356
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Search completed: March 29, 2003, 15:19:14 Job time : 104 secs RAR-alpha Clone la DNA encoding novel RAR-alpha A03 domi RAR-alpha RNA sequ RAR-alpha DNA sequ Clone pGEM-hRARgam

AAS83808

AAQ81

AAT33260

1481

1576 1903 1903 2521 2740 1913

clone phRAR

AAQ81476

85.2 885.2 885.2 885.2 713.8 771.9 771.9 771.9 57.9

PML-RAR-alpha RNA

Encodes human Reti Human retinoic aci Mouse retinoic aci Mouse retinoic aci

Murine retinoic ac Encodes skin-speci Human RARbeta2 PCR Human FLAG RARbeta

10388

AA01

ABK37

1912 1375 1399 8887

9151 2992 2992 2992 2989 20512 595 1351 5838

Vector genome plas Vector genome plas Human liver hap cD

Human liver hap cD

Genomic DNA encodi

Human hepatoma ret Human Hap (hepatom CDNA sequence #614

Human liver RAR-be Human EST-derived

Nucleotide sequenc DNA encoding novel DNA encoding novel

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1089.2
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1500.8
1500.8
1499.4
1207.6
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701.2
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667.8
648.8
591.4
552
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(without alignments)
12045.304 Million cell updates/sec
                                                                                                                                                  /SIDSZ/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
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/SIDSZ/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
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/SIDSZ/gcgdata/geneseqn-embl/NA1989.DAT:*
/SIDSZ/gcgdata/geneseqn-embl/NA1989.DAT:*
                                                                        March 29, 2003, 09:44:04 ; Search time 390 Seconds
      version 5.1.4_p5_4578 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                           2185239 seqs, 1125999159 residues
                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                  nucleic search, using sw model
                                                                                                                                                                          IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
      GenCore
Copyright (c) 1993
                                                                                                                                                                                                                                                                                                                                                     N_Geneseq_101002:*
                                                                                                                                                                                                                                                              length: 0
length: 2000000000
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2086
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                                                                                                                          Title:
Perfect score:
                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                           Minimum DB
Maximum DB
                                                  OM nucleic
                                                                                                                                                   Sequence:
                                                                                                                                                                                                              Searched:
                                                                                                                                                                                                                                                                                                                                                  Database
                                                                           Run on:
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ALIGNMENTS

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/product- "Human nuclear hormone receptor protein"
                                                                                    Human nuclear hormone receptor; therapeutic agent; gene therapy; immune response; gene; ss.
                                                                 cDNA encoding human nuclear hormone receptor protein.
                                                                                                                                 Location/Qualifiers
127..1500
/*tag= a
          AAL38338 standard; cDNA; 2086 BP
                                                                                                                                                                                                                   05-OCT-2001; 2001WO-US31095
                                                                                                                                                                                                                                     11-OCT-2000; 2000US-239117P
19-OCT-2000; 2000US-0691220
                                              15-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                  (PEKE ) PE CORP NY
                                                                                                                                                                            WO200231146-A2
                                                                                                               Homo sapiens
                                                                                                                                                                                                18-APR-2002.
                            AAL38338;
AAL38338
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*/

/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1997.bAT:*/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1998.bAT:*/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.bAT:*

/SIDS/gcgdata/geneseq/geneseqn.embl/NA1992.DAT:*/SIDS2/gcgdata/geneseq/geneseqn.embl/NA1993.DAT:*/SIDS2/gcgdata/geneseq/geneseqn.embl/NA1994.DAT:*/SIDS2/gcgdata/geneseq/geneseqn.embl/NA1994.DAT:*/SIDS2/gcgdata/geneseq/geneseqn.embl/NA1995.DAT:*/SIDS2/gcgdata/geneseq/geneseqn.embl/NA1995.DAT:*/SIDS2/gcgdata/geneseq/geneseqn.embl/NA1995.DAT:*/SIDS2/gcgdata/geneseq/geneseqn.embl/NA1995.DAT:*

/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*

Beasley EM;

Di Francesco V,

Ketchum KA,

Yan C,

٦,

Wei M,

myl/RAR-alpha fusi Human PML/RARalpha Human myl/RAR-alph Human PML/Alpha-RA

AAQ29334 AAV20474 AAV64990 AAA38656 AAT33259 ABK84517 ABL65214 AAV64991

24 113 24 24 20 20 20 20 20

2086 3036 3036 3036 3511 3511 2907 2907

85.4 85.4 85.4 85.3 85.3 85.3 85.3

1782.2 1782.2 1782.2 1782.2 1779 1779 1778.8 1778.8

CDNA encoding huma

AAL38338

100.

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Query Match Length

Score

٠ 9 Result

Description

PML-RAR-alpha DNA Human cDNA differe Lung cancer relate Human RAR-alpha cD

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The invention relates to an isolated peptide of a novel human nuclear hormone receptor with a fully defined sequence of 457 amino acids given in the specification. The novel human nuclear hormone receptor peptides and nucleic acids encoding them can be used as models for the development of human therapeutic cof human therapeutic targets, aid in the identification of therapeutic of human therapeutic cof human therapeutic cof human therapeutic cofficients, and stryers for the development of human therapeutic agents that modulate nuclear hormone receptor activity in cells and tissues that express the nuclear hormone receptor. The nucleic acids may be used as a query sequence to perform searches against sequence of databases to identify family members or related sequences, as probes or primers, to construct recombinant vectors, to identify compounds that modulate nuclear hormone receptor nucleic acid expression, in gene therapy, and as antisense constructs to control nuclear hormone receptor constructs to control nuclear hormone response, as a reagent in used to raise antibodies or to elicit an immune response, as reagent in assays designed to determine protein levels in biological fluids, as constructly a binding partner/ligand to develop a system for the identify abinding reaction, in drug screening assays, and to identify compounds that modulate protein in drug screening protein receptor construct reverse to the human nuclear construction of the human nuclear construction of the human nuclear construction in the human nuclear construction in the protein construction of the nuclear construction in the nuclear construction is expressed. New human nuclear hormone receptor proteins and nucleic acids, useful as models or targets for developing human therapeutic targets, and in identifying therapeutic proteins and modulators of nuclear hormone protein of the invention Claim 1; Fig 1; 73pp; English. New human nuclear hormone expression P-PSDB; AA021489 hormone receptor receptor

Sequence 2086 BP; 437 A; 685 C; 583 G; 381 T; 0 other;

180 240 180 300 300 360 360 420 420 480 540 9 9 Gaps **AACAGCACGAGGGGAGGTCTCTCTCCCCCAGCTGCTCTGCTCGGATGGCGCCG** GATTTTTATAACCAGAACCGGGCCTGTTTGCTCCCAGAGAAGGGGCTCCCCGCCCCGGGT CCGTACTCCACCCCGCTCCGGACTCCGCTTTGGAATGGCTCAAACCACTCCATTGAGACC GCCTGTGAGGGCTGCAAGGGCTTCTTCCGCCGCAGCATCCAGAAGAACATGGTGTACACG TGTCACCGGGACAAGAACTGCATCATCAAGAAGGTGACCCGGAACCCCTGCCAGTACTGC ATCTACAAGCCTTGCTTTGTCTGTCAGGACAAGTCCTCAGGCTACCACTATGGGGTCAGC GCCTGTGAGGGCTGCAAGGGCTTCTTCCGCCGCAGCATCCAGAAGAACATGGTGTACACG DB 24; Length 2086, Indels ; 0 Mismatches Pred. No. 0; Query Match 100.0%; Score 2086; Best Local Similarity 100.0%; Pred. No. 0; Matches 2086; Conservative 0; Mismatches 181 241 241 181 301 361 481 301 361 421 421 g ò 셤 g g ð ò ò ò g ò . <u>유</u> ò 음 ö g ò

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us-09-691-220-1.rng

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                                                                                                                                                                                                                                       (RAR)-alpha and myl which is characteristic of acute promyelocytic leukemia (APL). This is caused by a translocation of a portion of the long arm of chromosome 15 onto the long arm of chromosome 15 (t(15;17)(q21;q11-22)]. The breakpoint region has been cloned and has been shown that DNA rearrangements are clustered in the region of the first intron of RAR-alpha. This sequence was isolated by polymerase chain reaction (PCR) using primers which correspond to sequences both 5' and 3' to the breakpoint region.
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                                                                                                                                                                                                                    The sequence given shows a fusion between retinoic acid receptor
                                                       Marker for acute promyelocytic leukaemia and other neoplasias comprising nucleic acid and encoded abnormal retinoic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3036 BP; 605 A; 1018 C; 890 G; 523 T; 0
                                                                                                                                                                Disclosure; Fig 4; 84pp; English
                                                                                                           receptor-alpha receptor
P-PSDB; AAR27533
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AAV20474

RESULT

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The present sequence represents an oncogene from the present invention. The present invention describes a composition which comprises two antisense oligonuclectides. The first oligonuclectide is specific for a cytoplasmic oncogene or proto-oncogene selected from ras, raf. EGF-1, c-fms, c-ros, c-kit, c-met, c-trk, c-src, c-abl, bcr-abl, c-fgr and c-yes. The second oligonucleotide is specific for a nuclear oncogene or proto-oncogene selected from myc, jun, c-ets, c-fos, c-myb, B-myb, c-rel, c-vav, c-ski, c-spi, cyclin Dl, PML/RAR alpha, MLLI/MTG8, E2A/prl and ALL-1/AF-4. The composition is used for treating cancer. The combination of antisense oligonucleotides has synergistically enhanced ability to inhibit growth of cancer cells.
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99.8%; Pred. No. 0;
ive 0; Mismatches
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                                                                                                             Human; oncogene; proto-oncogene; ne
cancer; antisense oligonucleotide;
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This sequence encodes a human myl/RAR-alpha (retinoic acid receptor alpha) fusion protein which is used in a method for identifying a subject with acute promyelocytic leukaemia (APL) resulting from a t(15.17) translocation who will respond to treatment with all-trans retinoic acid. The protein can also be used to identify a subject with indications of APL who will not respond to treatment with all-trans
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The invention relates to modified human RNAse P external guide sequences (EGSs). The EGS is a ribozyme which forms the catalytic domain of the cribonucleoproteal RNAse P, which is involved in the processing of tRNA. The EGS comprises a cleavage targetting sequence and a recognition sequence which is complementary to the target RNA sequence. The crecognition arm which acceptor stem and the D stem of tRNA. The A recognition arm solocated at the 3' end of the EGS and the D at the 5' correspond to the aminoacyl acceptor stem and the D stem of tRNA. The A recognition arm is located at the 3' end of the EGS and the D at the 5' correspond to the modified nucleotide or an unmodified invention comprise at least one modified nucleotide or an unmodified deoxyribonucleotide, and the 3' end of the modified EGSs of the consist of the A and D arms, and the T stem and loop can consist of consist of modified The A and D arms, and the T stem and loop can consist of ribonucleotides with 5'-phosphate or 5'-phosphate or 5'-phosphorothioate linkages; or deoxyribonucleotides with 5'-phosphate or 5'-phosphate or 5'- phosphorothioate linkages; or deoxyribonucleotides with 5'-phosphate or 5'-phosphate or 5'- phosphorothioate linkages; or deoxyribonucleotides with 5'-phosphate or 5'-phosphate or 5'- phosphorothioate linkages. EGSs of the invention are used for cleaving a target RNA molecule. The invention discloses EGSs which are targetted conception at langer (HBV) RNA sequences, particularly hepatitis B curface antigen (HBAA) RNA, and EGSs targetted at PML/retinoic acid receptor alpha (RAR-alpha) fusion gene mRNA which is found in the majority of acute promple of the invention. The targetted EGSs used in an exemplification of the invention. The targetted EGSs used in an exemplification of the invention. The PML and the RAR-alpha gene fragments of che fusion gene is generated by a balanced reciprocal chromosomal translocation control procession of the fusion gene is always and procession of the fusion gene of the procession of the fusio
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catalytic RNA; antiviral; hepatitis B virus; HBV; anticancer; APL; acute promyelocytic leukaemia; retinoic acid receptor-alpha; RAR-alpha; PML; fusion gene; ss.
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96WO-US00513.
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/note= "base n at position 1477 is not identified
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PML-RAR-alpha DNA (AAT33259) is associated with acute promyelocytic leukaemia (APL). APL is characterised by a balanced, reciprocal translocation between the long arms of chromosomes 15 and 17. resulting in a fusion of the retinoic acid receptor gene (RAR-alpha and a gene for a putative transcription factor, PML. Methods for treating APL involve the use of ribozymes, external guide sequences and antisense oligonuclectices (see also AAT33245 and AAT33245.) the Specifically cleave the PML-RAR-alpha fusion mRNA (see also AAT33251) but not wild-type RAR-alpha mRNA. Plasmids carrying portions of the PML-RAR-alpha genes (see also AAT33260) allow synthesis of shortened versions of APL mRNA in vitro, facilitating testing and
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Matches 1782; Conservative
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The invention relates to detecting (MI) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (GS) identified by DNA chip analysis as given in the specification, and comparing the expression level to an expression level in an unactivated the expression level to an expression of GS is indicative of GCA.

CG, where differential expression of GS is indicative of GCA.

CG Also included are modulating (MZ) GA by contecting GC with an agent that alters the expression of at least one gene in GS; (2) screening (M3) content of GCA or an agent capable of modulating GCA or an inflammation (especially CCA or an agent capable of modulating GCA or an inflammation (especially CCA or an agent capable of modulating GCA or an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the CCA or an altergic response in a subject, exposure of a subject to a pathogen or sterile inflammaton; or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by contacting a tissue having or sterile inflammatory disease, by contacting a tissue having inflammation with an agent that modulates the expression of gene(s) from GS, where inflammation with an agent that modulates the expression of gene(s) from GS in the tissue. MI is useful for detecting an inflammation in a tissue, an allergic modulating GA; M3 is useful for screening an agent capable of modulating GA preferably in an inflammation in a tissue, an allergic detecting an allergic capable of modulating GA preferably in an inflammation in a tissue, an allergic capable of modulating capable of a subject.

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Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and drug toxicity
                                                                                                                                                                                                                                    Lry; ARDS;
bowel disease;
                                                                                                                                                                    Human cDNA differentially expressed in granulocytic cells #1088
                                                                                                                                                                                       Human; ss; granulocytic cell; DNA chip; bacterial infection; viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriasis; rheumatoid arthritis; glomerulonephritis; asthma; thrombosis; cardiac reperfusion injury; renal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel diseas Crohn's disease; ulcerative collitis; periodontal disease; granulocyte activation; chronic inflammation; allergy.
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response in a subject, exposure of a subject to a pathogen or steril inflammatory disease (e.g. psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, reperfusion injury, and inflammatory bowel disease, crohn's disease, ulcerative colitis, periodontal disease, also bacterial infection, viral infection, parasitic infection, protozoal infection, viral infection and M5 is useful for treating one of the above conditions. The present sequence represents a gene differentially expressed in granulocytes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic.
                                                                                                                                                                                                                                                                                                                                               CTATGGGGTCAGCGCTGTGAGGGCTGCAAGGGCTTCTTCCGCCGCAGCATCCAGAAGAA
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2907 BP

ABL65214; ABL65214;

ABL65214
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AC ABL

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RESULT

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                                                          stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
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                                               cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
1; lung; prostate; pancreas; carcinoma; antitumour; cancero
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene
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                             related gene sequence SEQ ID NO:3551
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200005-235280P.
200005-235637P.
200005-235711P.
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2000US-235077P.
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          (first entry)
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                             Lung cancer
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The present invention describes a method (MI) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of MI, and the data is sufficient to convey the chemical structure and/or properties of the agent. MI can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating ductal cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous cell cancinoma, neuroendocrine
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85.3%; Score 1778.8; DB 24; Length 2907;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 1786; Conservative 0; Mismatches 12; Indels 0; C
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                                                                                                                                                                                                                                                                                                 carcinoma, papillary carcinoma and Wilm's tumour.
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                                CCAGGACCTGGAGCAGCCGGACCGGGTGGAGTGCTGCAGGAGCCGCTGCTGGAGGCGCT
                                                AAAGGTCTACGTGCGGAAGCGGAGGCCCAGCCCCCCACATGTTCCCCAAGATGCTAAT
                                                                GAAGATTACTGACCTGCGAAGCATCAGCGCCAAGGGGGGCTGAGCGGGTGATCACGCTGAA
                                                                                                      GATGGAGATCCCGGGCTCCATGCCGCCTCTCATCCAGGAAATGTTGGAGAACTCAGAGGG
                                                                                                  CCACTCCCCGTGACCGCCCACGCCACATGGACACACCCCTCGCCCTCCGCCCCGGCTTTT
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This sequence encodes the human retinoic acid receptor alpha, RAR-alpha which is used in a method for identifying a subject with acute promyelocytic leukaemia (APL) resulting from a t(15:17) translocation who will respond to treatment with all-trans retinoic acid. The protein can also be used to identify a subject with indications of APL who will not respond to treatment with all-trans retinoic acid.
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                                                                                                                                                                  Fusion protein; myl; retinoic acid receptor-alpha; RAR; huma acute promyelocytic leukaemia; APL; t(15;17); translocation; treatment; all-trans retinoic acid; ss.
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/product= "RAR-alpha"
/note= "retinoic acid receptor-alpha"
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Best Local Similarity 99.3%; Pred. No. 0;
Matches 1786; Conservative 0; Mismatches
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P-PSDB; AAW81964.
                                    standard;
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CCAAG	CAGAAA H H H H H H H H H H	AACCAGO AACCAC	TCCCCTG TTCCCCCTG TTCCCCCTG TTCCCCCCTG TTCCCCCCCTG TTCCCCCCCC	96666T 9666GT 8666GT 8686GT 8686GT 8686GC 8686GC 8666GC
CTGCCAGTACTGCCGACTGCAGAAGTGCTTTGAAGTGGGCATGTCCAAGGAGTCTGTGAG	TCTGGACATGACCTGGGACAATACGACGACACAGGTCAGGACAGGTGTCTC TCTGGACATTGACTGGGACAAGTTCAGTGAACACAGGTGCATCAGGACACGTGTCTC TCTGGACATTGACCTCTGGGACAAGTTCAGTGAACTCTCCACCAAGTGCATCATTAAGAC TGTGGAGTTGACCTCTGGGACAAGTTCAGTGACTTCCACCAAGTGCATCATTAAGAC TGTGGAGTTGACCAAGCAGCTGCCCGGCTTCACCACCATCCACCATCGCCGACCAGTACAC TGTTGAAGTTGCCCAAGCAGCTGCCCGGCTTCACCACCACCATCGCCGACCAGATCAC TGTTGAAGTTCGCCAAGCAGCTGCCCGGCTTCACCACCACCATCGCGGACCAGATCAC TTTTTTTTTT	CGAGCAGGACACCATGACCTTCTCGGACGGGCTGACCCTGAACCGGACCCAGATGCACAA CGCTGGCTTCGGCCCCTCACCGACCTGGTTTTGCCTTTCGCCAACCAGCTGCTGCCCT		CCTGGACACTCTGAGCGGACACCGGGGGGGGGGGGGGGG
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/*tag= e
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/note= "RAR-alpha RNA"
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/note= "PML RNA"
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                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                    PML-RAR-alpha RNA (AAT33246) is associated with acute promyelocytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RNA construct(s) including ribozyme(s) and antisense oligo:nucleotide(s) - for the inactivation of RNA associated with, e.g. promyelocytic leukaemia or follicular lymphoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UGACGCCGGAGGUGGGGGAGCUCAUUGAGAAGGUGCGCAAAGCGCACCAGGAAACCUUCC
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                                                                                                                                                             leukaemia (APL). APL is characterised by a balanced and reciprocal translocation between the long arms of chromosomes 15 and 17, resulting in a fusion of the retinoic acid receptor gene (RAR-alpha, see also AAT33260) and a gene for a putative transcription factor, PML. Méthods for treating APL involve the use of ribozymes, external guide sequences and antisense oligonucleotides (see also AAT33245 and AAT33248-57) that specificleave the PML-RAR-alpha fusion mRNA (see also AAT33251) but not wild-type RAR-alpha mRNA.
                                                                                                                                                                                                                                                                                                          DB 17; Length 3511;
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s; Pred. No. 0;
325; Mismatches
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                                     Pace
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81.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence given represents the nucleic acid sequence of the retinoic acid receptor (RAR) alpha gene. This gene is disrupted in a translocation of a portion of the long arm of chromosome 17 onto the long arm of chromosome 15 [t(15;17)(q21;q11-22)]. This causes a fusion between RAR-alpha and myl which is characteristic of acute promyelocytic leukemia (APL). The breakpoint region has been cloned and it has been shown that DNA Rearrangements are clustered in the region of the first intron of RAR-alpha. This sequence was isolated by polymerase chain reaction (PCR). The primers used for amplification of this sequence can also be used to amplify the translocated region.
                                                                                                                                                                                               Retinoic acid receptor; RAR-alpha; myl; acute promyelocytic leukemia; APL; translocation; chromosome 17; chromosome 15; PCR; primer; [t(15;17)(q21;q11-22)]; breakpoint; polymerase chain reaction; ss.
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llarity 99.3%; Pred. No. 0;
Conservative 0; Mismatches 13; Indels 0;
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            Sequence 2928 BP; 582 A; 1012 C; 789 G; 545 T; 0 other;
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P-PSDB; AAR27534.
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Warrell RP;
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ATACCCTGCCATACCAACCCCAGGTATTAATTCTCGCTGGTTTTGTTTTTATTTTAATTT
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P-PSDB; AAP90395.
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                                                                       DNA of clone phRARI contg. the primary sequence of a protein (see corresp. AAP90395) that has ligand binding and transcription activating properties of retinoic acid receptor (RAR) protein. Used to make chimeric receptors, to produce receptor, to study binding complexes, and to screen
                                                                                                                                                                        DB 10; Length
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          DNA encoding retinoic acid receptor proteins - used to produce proteins for studying complexes ligands and in diagnostic assays.
                                                                                                                                                                       Score 1777.2;
Pred. No. 0;
0; Mismatches
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RAR-alpha clone lambda-KIR

(first entry)

01-SEP-1995

Location/Qualifiers 103..1491

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New haematopoietic stem cell lines with specific differentiation properties - made by transfected stem cells with nucleic acid encoding dominant negative suppressor of the retinoic acid receptor alpha, useful e.g. for haematopoietic reconstitution

Disclosure; Page 55-56; 100pp; English

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Collins SJ,

WPI; 1995-082227/11. P-PSDB; AAR68023.

94WO-US08450 93US-0099242

28-JUL-1994; 28-JUL-1993;

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                                                                                                                                                                                                                                                                                                                                     truncation of sequences coding for the C-terminal 59 amino acids and part the 3' UTR of the wild-type human sequence (AAQ81476). This truncated cDNA, designated RAR-alpha-403, encodes a protein (AAR68024) containing the N-terminus, DNA-binding domain and part the hormone-binding domain of RAR-alpha (AAR68023).
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Pred. No. 0;
0; Mismatches
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Best Local Similarity 99.3%;
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) are useful for treating
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                                                                                                                                                                                                                                                                                                                                                                                                                      Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                               encoding novel human diagnostic protein #18851.
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2000US-0649167.
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disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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Pred. No. 2.2e-309;
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Conditional sequences of the invention of mutations coding sequences of the invention but as seasons because of the invention of specification, but was obtained in electronic format directly from WIPO continuations.
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                                                                        forensic;
                                                                    e mapping; gene mapping; gene therapy; forensic,
medical imaging; diagnostic; genetic disorder;
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                                             novel human diagnostic protein #18852
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2000US-0649167
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Search completed: March 29, 2003, 13:27:12 Job time : 447 secs

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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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2054640 seqs, 14551402878 residues

Searched:

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Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKF2); Email s. Wiemann@dkfz-heidelberg.de; Sequenced by EMBL (European Molecular Biology Laboratories, Heidelberg/Germany) within the cDNA sequencing consortium of the German Genome Project.
This clone (DKF2P/GIC0417) is available at the R2DD in Berlin. Please contact the R2DD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at http://mips.gsf.de/proj/cDNA/.
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                                                                                           /organism="Homo sapiens"
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/tissue_type="amygdala"
/clone_lib=761 (synonym: had DH10B; sites Not1 + SalI"
/dev_stage="adult"
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Pred. No. 0;
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Email. nih.gov

Tissue Procurement: ATC Rubin Laboratory

CDNA Library Preparation: Rubin Laboratory

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing Dy: National Institutes of Health Intramural

Sequencing Center (NISC),

Gaithersburg, Maryland;

Web site:

http://www.nisc.nih.gov/

Contact:

nisc_medGahgrin.hgov/

Contact:

Netherby, K.D. Beckfrom-Sternberg, S.M.,

Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,

Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,

Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,

McDowell,J., Pearson,R., Sinder,B., Stantripop,S., Thomas,P.J.,

Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens, retinoic acid receptor, alpha, clone MGC:1651
IMAGE:3163891, mRNA, complete cds.
BC008727
MGC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2441)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (25-MAY-2001) National Institutes of Health, Mammalian
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Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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                                  TGACAGAGGGGTGGGACAGGGGGGGGGGTTCCCCCTGTACATACCCTGCCATACCAAC 1985
                  TGCCCAGCTCACCACATCTTCATCACCAGCAAACGCCAGGACTTGGCTCCCCCATCCTCA 1865
                                                                                      2206 CCCAGGTATTAATTCTCGCTGGTTTTGTTTTAATTTTTAATTTTTGTTTTGTTTTTTT 2265
                                                                                                    2086 GAACTCACAAGCCATTGCTCCCCAGCTGGGGAACCTCAACCTCCCCCCTGCCTCGGTTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC Project URL: http://mgc.nci.nih.gov
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ERVITLKMETPGSWPPLIQEMLENSEGLDTLSGQPGGGGRDGGGLAPPPGSCSPSLSP
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'note="Vector: pOTB7"
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~ u		108 GGAGATGGATGACGGGAGACGGGGCTGCTCAGCGCCATCTGCCTCATCTGCGGAGACG	ACCESSION ARÔ61121 VERSION ARO61121. KEYWORDS .	н
0 1		NGGACCTGGAGCAGCGGGACGGGTGGACATGCTGCAGGAGCCGCTGCTGGAGGCGCT 	<u>~</u>	ified.
о п		AAAGGTCTACGTGCGGAAGCGGAGGCCCAGCCCCCCACATGTTCCCCAAGATGCTAAT 1 	AUTHORS Dmitrovsky, E. TITLE Methods for c JOURNAL Patent: US 58 FEATHERS	sky, E. for c US 58
		GAAGATTACTGACCTGCGAACCATCAGCGCCAAGGGGGCTGATGCGGGTGATCACGCTGAA 	urce UNT 605	1 /org
5 1	Oy 1 Db 1	GATGGAGATCCCGGGCTCCATGCCGCCTCTCATCCAGGAAATGTTGGAGAACTCAGAGGG	tch al Simí 1784;	.larity Conserva
G 1	7 7	368 CCTGGACACTCTGAGCGGACAGCCGGGGGTGGGGGGCGGGGGGGG	Oy 290 CCATTGAGACCCAGA 	CCCAGA
0 0	1	.428 CCCGCCAGGCAGCTGTAGCCCCAGCCCCAGCTCCAACAGAAGCAGCCGGCCAC 1487 	Qy 350 CTCTACCCGGCATCT	SCATCT
0 11		488 CCACTCCCGGGACGCCCACGCCACATGGACACAGCCCTCGCCCTCCGCCCCGGCTTTT 1547	Qy 410 ATGGGGTCAGCGCT 	306001
. .		548 CTCTGCCTTTCTACCGACCATGTGACCCCGCACCAGCCCTGCCCCACCTGCCCTCCGG 1607	Qy 470 TGGTGTACACGTGTC 	SGTGTC
0 4		1608 GCAGTACTGGGGACCTTCCCTGGGGGAGGGAGGGAGCGACTCCTTGGACAG 1667 	Qy 530 GCCAGTACTGCCGAC	SCCGAC CCGAC
0 1		1668 AGGCCTGGGCCCTCAGTGGCTGCTCCCACAGCCTGGGCTGACGTCAGAGGCCGAG 1727 1111111111111111111111111111111111	Qy 590 ACGACCGAAACAAGA {	ACAAGA
J 11		1728 GCCAGGAACTGAGGCCCCTGGTCCTGGGTCTCAGGATGGGTCCTGGGGGCCTCGTG 1787 	Oy 650 TGACGCCGGAGGTGG 	AGGTGG \GGTGG
5 1		1788 TTCATCAAGACCCCTCTGCCCAGCTCACCACATCTTCATCACCAGCAACGCCAGGAC 1847 	Qy 710 CTGCCCTCTGCCAGC 	SCCAGO
5 11		848 TTGGCTCCCCCATCCTCAGAACTCACAAGCCATTGCTCCCCAGCTGGGGAACCTCAACCT 1907 	Qy 770 TGGACATTGACCTCT 	ACCTCT
5 1		908 CCCCCTGCCTCGCTTGGTGACAGAGGGGTGGGACAGGGGGGGG	Qy 830 TGGAGTTCGCCAAGC 	CAAGC 11111 CAAGC
5 1		1968 ATACCCTGCCATACCACCCAGGTATTAATTCTCGCTGGTTTGTTT	Oy 890 TCCTCAAGGCTGCCT 	TGCCT
5 4	Oy 2 Db 2	2027 TITIGITITGATITITITAATAAGAAITITCATITITAAGCACAAAAAAAAAA	QY 950 AGCAGGACACCATGA 	CATGA
			Qy 1010 CTGGCTTCGGCCCCC	೨೨೨೨೨

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ö PAT 29-SEP-1999 1010 CTGGCTTCGGCCCCTCACCGACCTGGTCTTTGCCTTCGCCAACCAGCTGCTGCCCTGG 1069 E., Warréll, R.P. Jr., Miller, W.H. Jr. and Frankel, S. detection of acute promyelocytic leukemia (APL) 5843642-A 1 01-DEC-1998; SCAGCTGCCGGCTTCACCACCCTCACCATCGCCGACCAGATCACCC 1849 469 649 769 829 709 SCAGCTGCCCGGCTTCACCACCTCACCATCGCCGACCAGATCACCC 889 TECCTEGACATCCTGATCCTGCGGATCTGCACGCGGTACACGCCCG 949 SAGCAGCAGTTCTGAAGAGATAGTGCCCAGCCCTCCCTCGCCACCCC 349 CTACAAGCCTTGCTTTGTCTGTCAGGACAAGTCCTCAGGCTACCACT 409 Gaps TETGAGGGCTGCAAGGGCTTCTTCCGCCGCAGCATCCAGAAGAACA CACCGGGACAAGAACTGCATCATCAACAAGGTGACCCGGAACCCCT SAAGAAGAAGGTGCCCAAGCCCGAGTGCTCTGAGAGCTACACGC SGGGGAGCTCATTGAGAAGGTGCGCAAAGCGCACCAGGAAACCTTCC SCTGGGCAAATACACTACGAACAACAGCTCAGAACAACGTGTCTCTC 2TGGGACAAGTTCAGTGAACTCTCCACCAAGTGCATCATTAAGACTG Length 3036; ö 3; Indels DB 6; Score 1782.2; DB 6 Pred. No. 7.2e-313; DNA u 0; Mismatches 523 3036 bp from patent US 5843642. cation/Qualifiers .3036 rganism="unknown" 1018 c 890 g GI:5988812 85.4%; 99.8%; to 3036) rative ŏ g

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Calabretta, B. and Skorski, T.
Antisense oligonucleotides targeting
Patent: US 5/34039-A 52 31 MAR-1998;
Location/Qualifiers
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PRI 08-JAN-1995

HUMPWLRAR 3036 bp mRNA linear Human PML-RAR protein (PML-RAR) mRNA, complete cds

DEFINITION

HUMPMLRAR LOCUS

RESULT 5

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HEARPLAELRNGSVREFLOGTRKTNNIFCSNFUNFPTLTSIYCRGCSRFLCSCALL
DSSHSELKCDISMEIQORGEELDAWTOALORDSAFGAVHAQNHAAVGGLGRARAETE
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VDMLQGFLLEALKVYVRKRRPSRPHHFPRMLMKITPLRSISARGAERVTTLKMEIFGS
MPPLIGEMLERNSEGLTLSGGGRGGGRDGGGLAPPPGGSCSPSLSSNRSSPATHSP"
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                                                                                                            Euteleostomi;
                                                                                                                           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3036)
Rakizuka,A., Miller,W.H. Jr., Umesono,K., Warrell,R.P. Jr.,
Frankel,S.R., Murty,V.V., Dmitrovsky,E. and Evans,R.M.
Chromosomal translocation t(15,17) in human acute promyelocytic
leukemia fuses RAR alpha with a novel putative transcription
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                                                                                                       Craniata; Vertebrata; E
Catarrhini; Hominidae;
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Pred. No. 7.2e-313;
); Mismatches 3;
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/cell_type="bone marrow"
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chromosome t(15;17) translocation
M73779.1 GI:190124
PML-RAR protein; fusion protein.
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/db_xref="taxon:9606"
                                                                                                       Eukaryota; Metazoa; Chordata;
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                                                                                                                                                                                                                                                                              factor, PML
Cell 66 (4), 663-674 (1991)
91347368
1652368
                                                   Homo sapiens cDNA to mRNA
Homo sapiens
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67. .2460
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ठे ठ		TGACGCCGGAGGTGGGGGGAGCTCATTGAGAAGGTGCGCAAAGCGCACCAGGAAACCTTCC 709	
2	2	CCCCARGO GGGGGGGGCTCATTGAGAGGTGCGCAAAAGCGCAACAACAAAAAAAA	
Qy Db	710	CTGCCCTCTGCCAGCTGGGCAAATACACTACGAACAACAGCTCAGAACAACGTGTCTCTC 769 	
δ d	770	TGGACATTGACCTCTGGGACAAGTTCAGTGAACTCTCCACCAAGTGCATCATTAAGACTG 829 	
3 6	າຕ	889	
· 6	Ō		
οy	890	49	
Q	1850	TCCTCAAGGCTGCCTGGACATCCTGATCCTGCGGATCTGCACGCGGTACACGCCCG 1909	
b 2y	950	AGCAGAACACCATGACCTTCTGGAACGGGCTGACCGTGAACGGGACCCAGATGCACAACG 1009 	
م م	1010	CTGGCTTCGGCCCCTCACCGACCTGGTCTTTGCCTTCGCCAACCAGCTGCTGCTGG 1069	
3 .	0.61	, ,	
6 6 6	1070	AGATGGATGGATGGGGGGGGTGCTCAGGGCCATCTGCTCATCTGGGAGAGGGGCTGCT 1129 	
ý 4	1130	AGGACCTGGAGCAGCCGGGCGGGCGGACTGGACGAGGAGCCGCTGCTGGAGCGCTAA 1189 	
3 8	1190	ATGCTAATGA 124	
g ģ	2150	20	
Qy Db	1250	AGATTACTGACCTGCGAAGCATCAGCGCCAAGGGGGCTGAGCGGGGTGATCACGCTGAAGA 1309 	
ò	1310	TGGAGATCCCGGGCTCCATGCCGCCTCTCATCCAGGAAATGTTGGAGAACTCAGAGGGCC 1369	
S 8	27	32	
Oy Dp	1370	TGGACACTCTGAGCGGACAGCCGGGGGGGGGGGGGGGGG	
δ	43		
Q C	3	AGGCAGCTGTAGCCCCCAGCCTCAGCCCCAACAGAAGCAGCCCGGCCACCCCCAACAGCAGC	
9 9	1490	ACTCCCGGTGACCGCCCACGCCCATGGACACAGCCTTCGCCCCCGGCTTTTCT 1549	
Οy	1550	CTGCCTTTCTACCGACCATGTGACCCCGCACCAGCCCTGCCCCGCACCTGCCCTCCGGGGC 1609	
qq	2510	THE THE TRANSPORT OF TH	
δλ	61	AGTACTGGGGACCTTCCCTGGGGACGGGAGGGAGGAGCACGCAC	
දු	2570	AGTACTGGGGACCTTCCCTGGGGGACGGGGGGGGGGGGG	
ري م	1670	GCCTGGGCCCTCAGTGGACTGCCTGCTCCCAAAGCCTGGGCTAAAGGCCGAGGC 1729 	
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Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G., Horrigan, S., Soppet, D.R. and Weaver, Z. Cancer gene determination and therapeutic screening using signature
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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           2690 CAGGAACTGAGTGAGGCCCCTGGTCCTGGGTCTCAGGATGGGTCCTGGGGCCTCGTGTT
                                             CATCAAGACACCCCTCTGCCCAGCTCACCACATCTTCATCACCCAGCAAACGCCAGGACTT
                                                       2750 CATCAAGACACCCCTCTGCCCAGCTCACCACATCTTCATCACACCAAACGCCAGGACTT
                                                                                                                                                                                 Score 1778.8; DB 6; Length 2907;
Pred. No. 3e-312;
0; Mismatches 12; Indels 0;
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Patent: WO 0194629-A 3551 13-DEC-2001;
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/db_xref="taxon:9606"
1011 c 789 g 546
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Best Local Similarity 99.3%;
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                                       AAACGACCGAAACAAGAAGAAGAAGGAGGTGCCCAAGCCCGAGTGCTCTGAGAGCTACAC
                   TCTGGACATTGACCTCTGGGACAAGTTCAGTGAACTCTCCACCAAGTGCATCATTAAGAC
                                                                                                    CGCTGGCTTCGGCCCCCTCACCGACCTGGTCTTTGCCTTCGCCAACCAGCTGCTGCCCCCT
                                                                                                                        TGTGGAGTTCGCCAAGCAGCTGCCCGGCTTCACCACCTCACCATCGCCGACCAGATCAC
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CHOLPVGGYSTPSPATIETGSSSSEEIVPSPPSPPPLPRIYKPCFVCQDKSSGYHYGV
SACEGKGFFRSIQKNMYYTCHRDKNTINKYTRNCOYCHACKACKOSKSKYN
BANGKKKEVPRPECSEXTLIPEVGELIEKVRKAHQETFPALCQLGKYTTNNSSEQRV
SLDIDLMDKFSELSTKCIIKTVFFARQLFGFTLTIADQITLLKRACLDIILIKRICTF
YTPEQDTMTFSDGLTLNRTQMHNAGFGPLTELVFAFANQLLPLEMDDAETGLLSAICL
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Banlahmad,A., Kohne,A.C. and Renkawitz,R.
A transferable silencing domain is present in the thyroid hormone receptor, in the v-erbA oncogene product and in the retinoic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Euteleostomi;
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AGGCCTGGGCCCTCAGTGGACTGCCTGCTCCACAGCCTGGGCTGACGTCAGAGGCCGAG 1727
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                                                                                                                                                                         TIGGCICCCCCATCCTCAGAACTCACAAGCCATTGCTCCCCAGCTGGGGAACCTCAACCT
                                                                                                                                                                                                                                                                                          receptor (AA 1-462)"
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
I (bases 1 to 290.E.S., Segui, P. and Evans, R.M.
Giguere, V., Ong, E.S., Segui, P. and Evans, R.M.
Identification of a receptor for the morphogen retino
8065922 (6149), 624-629 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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/db_xref="GI:36157"
/db_xref="SWISS-PROT:P10276"
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1. .2907
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="lambda hKIR"
/clone=llambda pKIR"
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/004e="put. retinoic acid re
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                                                                                        CCCTCTACCCCGCATCTACAAGCCTTGCTTGTCTGTCAGGACAAGTCCTCAGGCTACCA
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Thompson,C.C. Retinoic acid receptor c ligands Patent: EP 0325849-A2 1 Location/Qualif	1012 c 788 g	ch 1 Similarity 99.3%; Pred. No. 6e-312; 785; Conservative 0; Mismatches 13; Indels 0; Gaps 0;	CTCCATTGAGACCCAGAGCAGCAGTTCTGAAGAGATAGTGCCCAGCCCTCCCT	CCCTCTACCCCGCATCTACAAGCCTTGCTTGTCTGTCAGACAAGTCCTCAGGCTACCA 407 	CTATGGGGTCAGCGCCTGTGAGGGCTGCAAGGGCTTCTTCCGCCGCAGCATCCAGAAGAA 467 	CATGGTGTACACGTGTCACCGGGACAAGAACTGCATCATCAAGAGGTGACCCGGAACCC 527	CTGCCAGTACTGCCGACTGCAGAAGTGCTTTGAAGTGGGCATGTCCAAGGAGTCTGTGAG 587 	aaacgaccgaaacaagaagaagagggccccaagcccgagtgctctgagagctacac 647 	GCTGACGCCGGAGGTGGGGGAGCTCATTGAGAAGGTGCGCAAAGCGACCAGGAAACCTT 707 	CCCTGCCCTCTGCCAGCTGGGCAATACACTACGAACAACAGCTCAGAACAACGACGTGTCTC 767	TCTGGACATTGACCTCTGGGACAAGTTCAGTGAACTCTCCACCAAGTGCATCATTAAGAC 827 	TGTGGAGTTCGCCAAGCAGCTGCCCGGCTTCACCACCTCGCCGACCAGATCAC 887 	CCTCCTCAAGGCTGCCTGGACATCCTGATCCTGCGGATCTGCACGCGGTACACGCC 947 	CGAGCAGGACCATCATCGGACGGGCTGACCCTGAACCGGACCCAGATGCACAA 1007 	CGCTGGCTTCGGCCCCTCACCGACCTGGTCTTTGCCTTCGCCAACCAGCTGCTGCCCCT 1067	GGAGATGGATGCAGAGAGGGGGCTGCTCAGCGCCATCTGCCTCATCTGCGGGGACG 1127 	CCAGGACCTGGAGCAGCGGACCGGGTGGACATGCTGCAGGAGCGCTGCTGGAGGGCGCT 1187
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Tsai,S. and Collins,S.J.
Creating novel hematopoietic cell 1
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Patent: US 5830760-A 1 03-NOV-1998;
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<pre>5, K.M., Giguere, V., Ong, E.S., Segui, P.S., Umesono, K. and 5son, C.C. 1t: WO 8905355-A 1 15-JUN-1989; Location/Qualifiers 1. 2940 /organism="unknown" 94 a 1013 c 787 g 546 t</pre>	85.2%; Score 1777.2; DB 6; Length 2940; larity 99.3%; Pred. No. 6e-312; Conservative 0; Mismatches 13; Indels 0; Gaps	CTCCATTGAGACCCAGAGCAGTTCTGAAGAGATAGTGCCCAGCCCTCCCT	CCCTCTACCCCGCATCTACAAGCCTTGCTTGTCTGTCCAGACAAGTCCTCAGGCTACCA 407 	CTATGGGGTCAGCGCCTGTGAGGGCTGCAAGGGCTTCTTCCGCCGCAGCATCCAGAAGAA 467 	CATGGTGTACACCGGCACAAGAACTGCATCATCAACAAGGTGACCGGAACCC 527 	CTGCCAGTACTGCCGACTGCAGAAGTGCTTTGAAGTGGGCATGTCCAAGGAGTCTGTGAG 587 	AAACGACCGAAACAAGAAGAAGAGGGGGGCCCAAGCCCGAGTGCTCTGAGAGCTACAC 647 	GCTGACGCCGGAGGTGGGGGAGCTCATTGAGAAGGTGCGCAAAGCGCACCAGGAAACCTT 707 	CCCTGCCCTCTGCCAGCTGGGCAAATACACTACGAACAACAGCTCAGAACAACGTGTCTC 767 	TCTGGACATTGACCTCTGGGACAAGTTCAGTGAACTCTCCACCAAGTGCATCATTAAGAC 827 	TGTGGAGTTCGCCAAGCAGCTGCCCGGCTTCACCACCTCCCACCATGGCCGACCAGATCAC 887 	CCTCCTCBAGGCTGCCTGGACATCCTGATCCTGCGGATCTGCACGCGGTACACGCC 947 	CGAGCAGGACCACCATGACCTTCGGACGGGCTGACCCTGAACCGGACCCAGATGCACAA 1007 	CGCTGGCTTCGGCCCCCTCACCGACCTGGTCTTTGCCTTCGCCAACCAGCTGCTGCCCCT 1067	GGAGATGGATGGATGCGGGAGACGGGGCTGCTCAGCGCCATCTGCCGTCATCTGCGGAGACCG 1127 	CCAGGACCTGGAGCAGCGGGTGGACATGCTGCAGAGCCGCTGCTGGAGGCGCT 1187
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AUTHOKS JOURNAL FEATURES SOURCE BASE COUNT	Query Ma Best Loc Matches	Qy 288 Db 279	Qy 348 Db 339	Oy 408 Db 399	Oy 468 Db 459	Oy 528 Db 519	Qy 588 Db 579	Qy 648 Db' 639	Qy 708 Db 699	Qy 768 Db 759	Qy 828 Db 819	Oy 888 Db 879	Qy 948 Db 939	Qy 1008 Db 999	Qy 1068 Db 1059	Oy 1128

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12 (bases 1 to 2008)

13 Isogal.T. and Yamamoto,J.

14 Elemaitsion

15 Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7

16 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan

17 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan

18 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan

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18 Facara-Kamatari, Facara-Kamatari, Chiba 10 Kamatari, Chiba 10 Kamatari, Chiba 10 Kamatari, Mational Institute of Technology and RAB; annotation: HRI and RAB;

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                               Suzuki,O., Sasaki,N., Aotsuka,S., Shoji,T., Ichihara,T., Shiohata,N., Matsumoto,K., Hirano,M., Sano,S., Nomura,R., Yoshikawa,Y., Matsumuta,Y., Moriya,S., Chiba,E., Momiyama,H., Onogawa,S., Kaeriyama,S., Satoh,N., Matsunawa,H., Takahashi,E., Tarashima,Y., Watanabe,M., Satoh,N., Matsunata,K., Takahashi,E., Sato,H., Char, Makamatsu,A., Ishi,S., Yammanco,T., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T., Irie,R., Otsuki,T., Matsuo,K., Nakamura,Y., Sekine,M., Kimura,Y., Yamashita,H., Wagatsuma,M., Murakawa,K., Kanehori,H., Kanda,K., Oshima,A., Sugiyama,A., Kanehori,K., Takahashi-Fujii,A., Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S., Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T., Sugano,S.,
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/db_xref="taxon:9606"
/clone="TRACH2015486"
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/clone_lib="TRACH2"
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KNMYYTCHROKNCIINKYTRNRCOYCRLOKCFPGUSKESVRUDRNKKKBYPKPPECS
ESYTLTPEVGELIEKVRKAHQETFPALCQLGKYTTNNSSEGRVSLDIDLMDKFSELST
KCIIKWYBFAKQLPGFTTLTIADQITLLKAACLDILLIKICTRYTPEQDTMTFSDGLI
LNRTQMHNAGFGPLTDLVFAFANQLLPLEMDDAETGLLSAICLICGDRQDLEQPDRVD
MLQDFULLEALKYYVRKRRPSRPHMFPKALMKTTDLRSISAKGAERVTTLKMETPGSMP
PLIQBFALEASSGRAYYVRKRRPSRPHMFPKALMKTTDLRSISAKGAERVTTLKMETPGSMP
PLIQBFALEASSGRAYGGGRAGGGGRAGGGGRAGGGRAPGGGRAPGGGRAPGGGRAPGGGRAPGGGRAPGGGRAPGGGRAPGGGRAPGGGRAPGGGRAPGGGRAPGGGRAPGGGRAPGGGRAPGFA
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RTVSLGAGAKDELHIVEAEAMNYEGSPIKVTLATLKMSVQPTVSLGGFEITPPVVLRL
KCGSGPVHISGQHLVAVEEDAESEDEEEEDVNRVLFMKPKGRGLKHMFGDLVCSWKLA
                                                                                                                                                                                                                                                                                                        HSU41742 2073 bp mRNA linear PRI 17-MAY-1996 Human nucleophosmin-retinoic acid receptor alpha fusion protein NPW RAR long form mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I Chases 1 to 2073)
Redner, R.L., Rush, E.A., Faas, S., Rudert, W.A. and Corey, S.J. The t(5;17) variant of acute promyelocytic leukemia expresses a nucleophosmin-retinoic acid receptor fusion
Blood 87 (3), 882-886 (1996)
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                                                                                                  GGAACCTCAACCTCCCCCCTGCCTCGGTTGGTGACAGAGGGGGTGGGACAGGGGCGGGGG
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fusion protein NPM-RAR long form"
/protein_id="AAB00112.1"
/db_xref="GI:1314308"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_type="acute promyelocytic le
t(5;17)(932;q11) translocation"
/tissue_type="bone marrow"
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Submitted (30-NOV-1995) Robert L. R
Pittsburgh, E1058 BST, 211 Lothrop
USA
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/bcrtein_id="CaA29787.1"
/db_xref="G1:35874"
/db_xref="SPOOT:P10276"
/translation="MLGGLSPPGALTTLOHOLPVSGYSTPSPATIETOSSSSEEIVPS
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WYTRNRQCYCRLQKCFFVGNKEEVRYRDKNKKKFWPPRESCESYTLPFEVGELIEK
VRKAHQFTPPALCOLGKYTTNNSSEDRVSLDIDLMDKFSELSFKCIIKTVEFAKQLPG
FTTLTIADOITLLKAACLDILLILRICTRYTPEODTMTFSDGLTLNRTOMHNAGFGPLT
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                        Petkovich,M., Brand,N.J., Krust,A. and Chambon,P. A human retinoic acid receptor which belongs to the family
                                                                                         CAGCCCCAGCTCCAACAGAAGCAGCCGGCCACCCACTCCCCGTGACCGCCCACGCCACA
                                                                                                                                                                                      CCGCACCAGCCCTGCCCTGCCCTCCCGGGCAGTACTGGGGGACCTTCCCTGGGGGA
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/note="retinoic acid receptor
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/db_xref="taxon:9606"
317. 1615
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Nature 330 (6147), 444-450 (1987)
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Chambon, P.
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X06538.1 GI:35873
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Pred. No. 1.1e-261;
0; Mismatches 7;
                                        488. .685
/note="put. DNA-binding domain"
763. .764
/note="gc was cg in [1]"
/citation=[1]
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/note="put. ligand-binding
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Best Local Similarity 99.5%;
Matches 1504; Conservative
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Redner, R.L.
Direct Submission
Submitted (30-NOV-1995) R
Pittsburgh, E1058 BST, 21, USA
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Matches 1503; Conservative
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1944)
Redner, R.L., Rush, E.A., Faas, S., Rudert, W.A. and Corey, S.J.
The t(5:17) variant of acute promyelocytic leukemia expresses a nucleophosmin-retinoic acid receptor fusion
Blood 87 (3), 882-886 (1996)
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CGCTGGCTTCGGCCCCCTCACCGACCTGGTCTTTGCCTTCGCCAACCAGCTGCTGCCCCCT 1182
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/codon_start=1
/product="nucleophosmin-retinoic acid receptor alpha
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/product="nucleophosmin-retinoic acid receptor alpha
fusion protein NPW RAR short form"
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RYGSGAGARDELHIVEABANNYEGEPIKVTATLKNSVQPTVSLGGFETTPPVVLRL
RYGSGAGARDELHIVEABANNYEGEPIKVTINKYTRNRCQYCRLQKCFEVQMSKESVRN
SACGGCKGFFRRSIGKNAYTTLPPEVGELIEKVRKAHQFFFPALCOLGKTYTNNSSEGRV
SLDIDLWDKFEREZSTKCITKTVEFAKQLDFTLTTADQITLLKAACLDILLIEGTR
YTPEQOTWTFSGGLTINRTQMHNAGGPLTLCLLYFFRANQMTFSGGRV
ICGDRQDLEQPDRYDMLQFELLEALKYYVRKRRPSRRHMFPRALMKITDLILLEICTR
ICGDRQDLEQPDRYDMLQFELLEALKYYVRKRRPSRRHMFPRALMKITDLIRGISAICL
ICGDRQDLEQPDRYDMLQFELLEALKYYVRKRRPSRRHMFPRALMKITDLIRGISAICL
ICGDRQDLEQPRALDLIGEMLENSEGDTLSGGGGGGGGGGGGGGGGGGSFLSP.
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  of
) Robert L. Redner, Medicine, University o
211 Lothrop Street, Pittsburgh, PA 15213,
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'Organism="Homo sapiens"

/db_xref="taxon:9606"

/cell_type="acute promyelocytic leukemia

+t(5:17)(q32;q11) translocation"

/tissue_type="bone marrow"
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        CTGGCTTCGGCCCCCTCACCGACCTGGTCTTTGCCTTCGCCAACCAGCTGCTGCCTGG
TGGAGTTCGCCAAGCAGCTGCCCGGCTTCACCATCATCATCGCCGAACCAGATCACCC
                               TCCTCAAGGCTGCCTGGCTGGACATCCTGTGCGGGATCTGCACGCGGTACACGCCCG
                                                                                                                                                                       1276 AGGACCTGGAGCAGCCGGACGGGTGGACATGCTGCAGGAGCGCTGCAGAGGCGCTAAA
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Search completed: March 29, 2003, 14:38:37 Job time : 4319 secs

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March 29, 2003, 05:30:18 ; Search time 62 Seconds
   (without alignments)
1518.767 Million cell updates/sec
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2437
1 MYESVEVGGPTPNPFLVVDF......SCSPSLSPSSNRSSPATHSP 457
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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                   671580 seqs, 206047115 residues
                                                                                     OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries sp_fungi:*
sp_human:*
sp_invertebrate:* SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:* Database :

ALIGNMENTS

sp_vertebrate:*
sp_unclassified:*
sp_unvirus:*
sp_bacteriap:*
sp_archeap:* sp_mammal:*
sp_mhc:*
sp_organelle:*
sp_phage:* sp_plant: *
sp_rodent: *
sp_virus: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Q9qwjl rattus norv	_	P97513 mus spretus	Q8vhb8 mesocricetu	Q92019 xenopus lae	Q90272 brachydanio	Q91391 brachydanio	Q90271 brachydanio	Q8vhb7 mesocricetu	Q910c7 coturnix co	O91yx2 mus musculu	_	Q8vhb6 mesocricetu	Q918t3 ambystoma m	Q918t2 ambystoma m	Q9qwt3 rattus norv
RIES	0	<u>`</u>	_	~ i													
SUMMARIES	ID	Q9QWJ1	015156	P97513	Q8VHB8	092019	090272	091391	090271	Q8VHB7	Q910C7	Q91YX2	091VK5	98ИНВ6	Q918T3	Q918T2	Q9QWT3
	DB	Ξ.	4	1	11	13	13	13	13	Π	13	11	11	1	13	13	11
	Query Match Length DB	459	797	462	430	448	457	444	444	448	448	458	458	443	441	446	307
æ	Query Match	96.4	86.7	82.8	85.0	83.2	82.9	82.4	82.0	72.6	72.2	67.7	67.7	67.6	67.3	8.99	66.5
	Score	2349	2112	2092	2072.5	2026.5	2021	2008.5	1998.5	1770	1760	1651	1651	1646.5	1641	1628.5	1620
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090968 gallus gall 09uj38 homo sapien 09073 brachydanio 09046 paralichthy 090y67 paralichthy 090y70 paralichthy 090y70 paralichthy 090y69 paralichthy 090y69 paralichthy 090y69 paralichthy 090y69 paralichthy 090y69 paralichthy 090y180 paralichthy 090y180 sus scrofa 090y13 homo sapien 090y21 salmo sapien 090y21 salmo salar 096594 avian eryth 090y21 salmo salar 096593 avian eryth 090y21 salmo salar 096591 avian eryth 090y31 dugu rubrip 091x41 mus musculu 091x41 mus musculu 091x41 aedes aegyp 091x41 aedes aegyp	
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MYYTCHRDKNCIINKVTRNPCQYCRLQKCFEVGMSKESVRNDRNKKKKEVPKPECSESYT 174
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            leukemia fuses RAR alpha with a novel putative transcription factor,
                                                                                                                                                                                                                                                                                                                                                                                                                           395 AIETQSSSSEEIVPSPPSPPPLPRIYKPCFVCQDKSSGYHYGVSACEGCKGFFRRSIQKN
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                                                                                                                                                                                                                                                                                                                   ONA-binding; Nuclear protein; Receptor; Transcription regulation;
                       797 AA; 89281 MW; 8C16B6E85CBDD214 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LDTLSGQPGGGRDGGGLPPPPGSCSPSLSPSSNRSSPATHSP 457
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Retinoic acid receptor-alpha.
 'Chromosomal translocation t(15;17) in human acute
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                                                                                                                                                                                                                                                                                                                                                                Score 2112; DB 4;
Pred. No. 2e-174;
1; Mismatches
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                                                                                                  SMART; SM00336; BBOX; 1.
SMART; SM00430; HOLI; 1.
SMART; SM00184; RING; 1.
PROSITE; PS00039; NUCLEAR_RECEPTOR; 1.
PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
PROSITE; PS00518; ZF_RING; 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                      1;
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99.3%;
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P97513;
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                                                                                                                                                                                                                                                                                                                   61 QSSSSEEIVPSPPSPPPLPRIXKPCFVCQDKSSGYHYGVSACEGCKGFFRRSIQKNMYYT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179 VGELIEKVRKAHQETFPALCQLGKYTTNNSSEQRVSLDIDLWDKFSELSTKCIIKTVEFA 238
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                                                                                                                                                                                                                                                                                                        QSSSSEEIVPSPPSPPLPRIYKPCFVCQDKSSGYHYGVSACEGCKGFFRRSIQKNMVYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             299 PLIDLVFAFANQLLPLEMDDAETGLLSAICLICGDRQDLEQPDRVDMLQEPLLEALKVYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           359 RKRRPSRPHMFPKMLMKITDLRSISAKGAERVITLKMEIPGSMPPLIQEMLENSEGLDTL
                                                                                                                          SMART; SM00430; HOLI; 1.
SMART; SM00399; ZnF_C4; 1.
PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
DNA-binding; Nuclear protein; Receptor; Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY
                                                                                                                                                                                                                                      ;
;
                                                                                                                                                                                                             Length 459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
BEDLINE-1347368; PubMed-1652368;
Kakizuka A., Miller W.H. Jr., Umesono K., Warrell R.P. Jr.
Frankel S.R., Murty V.Y., Dmitrovsky E., Evans R.M.;
                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                      459 AA; 50928 MW; F03368934C1E3C86 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                            96.4%; Score 2349; DB 11;
96.9%; Pred. No. 2.7e-195;
11ve 4; Mismatches 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        797
                              InterPro; IPR0010536; Hormone_rec_lig.
InterPro; IPR001023; Stdhrmm.receptor.
InterPro; IPR001028; Znf_C4steroid.
Pfam; PP00104; hormone_rec; 1.
Pfam; PF00105; zf-C4; 1.
PRINTS; PR00398; STRDHORMONER.
PRINTS; PR00047; STROIDEINGER.
PRINTS; PR00047; STROIDEINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
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21,
         EMBL; U15211; AAC23439.1;
HSSP; P10826; 1HRA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     015156 PRELIMINARY;
015156;
01-NOV-1996 (TYEMBLEEL) 0.
01-NOV-1996 (TYEMBLEEL) 0.
01-JUN-2002 (TYEMBLEEL) 2.
PML-RAR PIOCESIN.
                                                                                                                                                                                                                                    Matches 445; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                           Zinc-finger
SEQUENCE
                                                                                                                                                                                                             Query Match
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Gaps

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Indels

574

634 354 430 AA

PRT;

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us-09-691-220-2.rspt

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PRELIMINARY;
                                                                                                   NCBI_TaxID=10036;
                                                                                                                                                                                                                                                                                              Receptor.
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                                                                                                                                                                                                                                                                                                                                     Local
            98 УНВ
                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                  MEDLINE-98134036; PubMed-9473767; Gariboldi M., Vivat V., De Gregorio L., Manenti G., Chiariello E., Falvella F.S., Pierotti M.A., Dragani T.A.; Analysis of the retinoic acid receptor alpha gene as a candidate for the pulmonary adenoma resistance 1 gene."; Mol. Carcinog. 21:13-16(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127 INKVTRNPCQYCRLQKCFEVGMSKESVRNDRNKKKKEVPKPECSESYTLTPEVGELIEKV 186
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                                                                                                                                                                                                                                                                                                                                                                                   7 VGGPTPNPFLVVDFYNQNRACLLPEKGLPAPGPYSTPLRTPLWNGSNHSIETQSSSSEEI 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RKAHQETFPALCQLGKYTTNNSSEQRVSLDIDLWDKFSELSTKCIIKTVEFAKQLPGFTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FANOLLPLEMDDAETGLLSAICLICGDRODLEQPDRVDMLQEPLLEALKVYVRKRRPSRP
Mus spretus (Western wild mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                 SMART; SM00430; HOLI; 1.

SMART; SM00399; ZnF_C4; 1.

PROSITE; PS00011; NUCLEAR RECEPTOR; 1.

Zinc-finger. 30 S -> P.

VARIANT 30 S -> P.
                                                                                                                             -i- SUBCELLUIAR LOCATION: NUCLEAR (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY EMBL; Y10094; CAA71177.1; -HSSP; P10826; IHRA.
                                                                                                                                                                                                                                                                                                                                                                20;
                                                                                                                                                                                                                                                                                                                                            Length 462;
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                                                                                                                                                                                                                                                                                                    S -> P.

E -> D.

47475F78C6FE1ACA CRC64;
                                                                                                                                                                                                                                                                                                                                          85.8%; Score 2092; DB 11;
90.2%; Pred. No. 5.2e-173;
1ve 7; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RDGGGLPPPPGSCSPSLSPSSNRSSPATHSP 457
                                                                                                                                                                    InterPro; IPR000536; Hormone_rec_lig.
InterPro; IPR001723; Stdhrmn_receptor.
InterPro; IPR001628; Znf_c4steroid.
Pfam; PF00104; hormone_rec; 1.
Pfam; PF00105; zf-c4; 1.
                                                                                                                                                                                                                     PRINTS; PR00398; STRDHORMONER.
PRINTS; PR00047; STROIDFINGER.
ProDom; PD000035; Znf_C4steroid; 1.
                                                                                                                                                                                                                                                                                                    30 S
150 E
50739 MW;
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                                                           STRAIN-SPAIN; TISSUE-LUNG;
                                                                                                                                                                                                                                                                                                                                                              Matches 407; Conservative
                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                             150 1
462 AA;
                                                SEQUENCE FROM N.A.
                            NCBI_TaxID=10096;
                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                              VARIANT
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RESULT O8VHB8

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SEQUENCE FROM N.A.
Sharma R.P., McGraw R.A., Dugyala R.R.;
"Cloning and characterization of hamster fetal retinoic acid receptor isoforms.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY046943; AAL02360.1; -.
InterPro; IPR001723; Stuhrmn_receptor.
InterPro; IPR001723; Stuhrmn_receptor.
InterPro; IPR001628; Zuf_C4steroid.
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                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 11; Length 430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         430 AA; 47466 MW; 48A924167E105646 CRC64;
01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNI-2002 (TrEMBLrel. 21, Last annotation update)
Retinoic acid receptor alpha.
Mesocricetus auratus (Golden hamster).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85.0%; Score 2072.5; DB 11
93.0%; Pred. No. 2.3e-171;
tive 5; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00031; NUCLEAR RECEPTOR; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00398; STRDHORMONER.
PRINTS; PR00047; STROIDFINGER.
PRODOM; PR000035; Znf_C4steroid; 1.
SMART; SM00430; HOLI; 1.
SMART; SM00399; ZnF_C4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00104; hormone_rec; 1 Pfam; PF00105; zf-C4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       400; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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HRSSPATQSP 430
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--GGASSQTPVTPVAPGSCSPSLSPSSTHSSPSSHSP
                                                                                                                                                              SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                        TISSUE-EMBRYO;
Stachel S.E.;
                                                                                                                                                                        TISSUE-EMBRYO;
                                                                      01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Simi
Matches 378;
                                                                                                                                                                                                                                                                                                                                                                                                                             Zinc-finger
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                     090272
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                                                                                                                  "Two isoforms of retinoic acid receptor alpha expressed during Xenopus development respond to retinoic acid."; Mech. Dev. 39:81-93(1992).
                                                                                                                                                                                                                                                                                                                                                                                                        61 SSSEEIVPSPPSPPPLPRIYKPCFVCQDKSSGYHYGVSACEGCKGFFRRSIQKNMVYTCH 120
                                                                                                                                                                                                                                                                                                                                                                                                                121 RDKNCIINKVTRNPCQYCRLQKCFEVGMSKESVRNDRNKKKKEVPKPECSESYTLTPEVG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 ELIEKVRKAHQETFPALCQLGKYTTINNSSEQRVSLDIDLWDKFSELSTKCIIKTVEFAKQ 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 LPGFTTLTIADQITLLKAACLDILILRICTRYTPEQDTMTFSDGLTLNRTQMHNAGFGPL 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                           54
                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                              PROSITE; PS00031; NUCLEAR RECEPTOR; 1.
DNA-binding; Nuclear protein; Receptor; Transcription regulation;
Zinc-finger.
                                                                                                                                                         DB 13; Length 448;
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م
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                                                                                                                                                                                                                                                                                                                        6CF94B31BC57054B CRC64;
        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                       83.2%; Score 2026.5; DB 13
84.9%; Pred. No. 2.4e-167;
-1ve 22; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPGGGGRDGGGLPPPGSCSPSLSPSSNRSSPATHSP 457
                                        Kenopus laevis (African clawed frog).
  Created)
                                                                                                                                                                                                                                                   PRINTS; PR00398; STRDHORMONER.
PRINTS; PR00047; STROIDFINGER.
PRODOM; PD000035; ZNf_C4steroid; 1.
SMART; SM00430; HOLI; 1.
SMART; SM00399; ZnF_C4; 1.
                                                                                                   MEDLINE-93144180; PubMed-1336976;
                                                                                                                                                                                                                                                                                                                       448 AA; 50456 MW;
01,
21,
                                                                                                                                                                                                                                                                                                                                                al Similarity 84.93
388; Conservative
01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
        (TrEMBLrel.
                        Retinoic acid receptor
                                                                  Xenopus.
                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                         SEQUENCE FROM N.A.
                                                                         NCBI_TaxID=8355;
                                                                  Xenopodinae;
                                                                                                            C.R.;
                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                            Sharpe
                                                                                                                                                                                                                                                                                                                                                        Matches
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CHRDKNCIINKVTRNPCQYCRLQKCFEVGMSKESVRNDRNKKKKEVPKPECSESYTLTPE 178
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA-binding; Nuclear protein; Receptor; Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Retinoic acid reprograms RAR expression and shows anteroposteri
specification occurs in the pre-gastrula zebrafish.";
submitted (DEC-1992) to the EMBL/GenBank/DDBJ databases.
-1- SUBCELLULAR LOCATION: UNCLEAR (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                  "The molecular characterization of three zebrafish retinoic receptor genes suggests the retinoic acid pathway functions embryonic hindbrain development.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         embryonic hindbrain development.";
Submitted (DEC-1992) to the EMBL/GenBank/DDBJ databases.
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                                                                     01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Retinoic acid receptor alpha-2.B.
RARA2B OR RAR-ALPHA-2.B.
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EFIN: ZDB-GENE-980526.72; rara2b.

InterPro; IPR000536; Hormone_rec_lig.

InterPro; IPR001723; Stdhrmn_receptor.

InterPro; IPR001628; Znf_C4sterold.

Pfam: PF00104; hormone_rec; 1.

Pfam: PF00105; Zf-C4; 1.

PRINTS; PR00398; STRDHORMONER.

PRODOM; PD000035; Znf_C4sterold; 1.

SMART; SM00430; HOLI; 1.

PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
                                                      Created
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HSSP; P10826; 1HRA.
                                                                                                                                                                                                                                                                                                                                                                                                              Stachel S.E., Kushner P.;
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SEQUENCE FROM N.A.
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Joore J., van der Lans G.B., Lanser P.H., Vervaart J.M., Zivkovic D.,
Speksnijder J.E., Kruijer W.;
"Effects of retinoic acid on the expression of retinoic acid receptors
during zebrafish embryogenesis.";
Mech. Dev. 46:137-150(1994).
                                                                                                                                                                                       RKRRPSRPHMFPKMLMKITDLRSISAKGAERVITLKMEIPGSMPPLIQEMLENSEGLDTL 418
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinoptergyli; Neopterygil; Teleostel; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
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                   KOLPGFTTLTIADQITLLKAACLDILILRICTRYTPEQDIMTFSDGLTLNRTQMHNAGFG
                                                                                PLIDLVFAFANQLLPLEMDDAETGLLSAICLICGDRQDLEQPDRVDMLQEPLLEALKVYV
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PRINTS; PRO047; STROHORNORR.
PRINTS; PRO0047; STROHOFINGER.
SMART; SM00439; HOLI; 1.
SMART; SM0039; ZDE_C4; 1.
PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
DNA-binding; Nuclear protein; Receptor; Transcription regulation;
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-1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
EMBL; S74155; AAB13276.1; -.
HSSP; P10826; 1HRA.
ZFIN; ZDB-GENE-990415-239; rara.
InterPro: IPR000536; HORMONE.rec_lig.
InterPro: IPR001723; Stdhrmn.receptor.
InterPro: IPR001628; Znf_C45teroid.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                         419 SGQPGGGRDGGGLPPPPGSCSPSLSPSSNRSSPATHSP 457
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Pfam; PF00105; zf-C4; 1.
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tes 379; Conserv
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Matches
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239
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233 LPGFTTLTIADQITLLKAACLDILILRICTRYTPEQDTMTFSDGLTLNRTQMHNAGFGPL 292
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Brachydanio rerio (Zebrafish) (Zebra danio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                       Stachel S.E.;
"Retinoic acid reprograms RAR expression and shows anteroposterior specification occurs in the pre-gastrula zebrafish.";
Submitted (DEC-1992) to the EMBL/GenBank/DDBJ databases.
-! - SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-! - SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
                                                                                        ELIEKVRKAHQETFPALCQLGKYTTNNSSEQRVSLDIDLWDKFSELSTKCIIKTVEFAKQ
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DNA-binding; Nuclear protein; Receptor; Transcription regulation;
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"The molecular characterization of three zebrafish retinoic
receptor genes suggests the retinoic acid pathway functions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             413 AQGSRAS----ATTPGSCSPSLSPNSAQSSPPTQSP 444
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InterPro; IRR000536; Hormone_rec_lig.
InterPro; IRR00123; Stdhrmn_receptor.
InterPro; IRR001028; 2nf_C4steroid.
Pfam; PF00104; hormone_rec; 1.
Pfam; PF00105; zf-C4; 1.
PRINTS; PR00398; STRDHORMONER.
PRINTS; PR00047; STROIDFINGER.
ProDom; PD000035; Znf_C4steroid; 1.
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HSSP; P10826; 1HRA.
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SMART; SM00399; ZDF_C4;
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Mismatches

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'Cloning and characterization of hamster fetal retinoic acid receptor
                                                                        9
                                        Gaps
                                                                                                           52
                                                                                     ELIEKVRKAHQETFPALCQLGKYTTNNSSEQRVSLDIDLWDKFSELSTKCIIKTVEFAKQ
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                       13;
   DB 13; Length 444;
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                                       Indels
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EMBL, AY046944; AAL07361.1; -
InterPro; IPR000536; Hormone_rec_11g.
InterPro; IPR001723; Stdhrmn_receptor.
InterPro; IPR001628; Znf_C4steroid.
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNI-2002 (TrEMBLrel. 21, Last annotation update)
Retinoic acid receptor beta-2.
Mesocricetus auratus (Golden hamster).
                                     31;
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Pred. No. 4.2e-145;
                      6.4e-165;
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82.0%; Score 1998.5;
82.5%; Pred. No. 6.4e
ive 36; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00398; STRDHORMONER.
PRINTS; PR00047; STROIDFINGER.
ProDom; PD000035; Znf_C4steroid; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00104; hormone_rec; 1. Pfam; PF00105; zf-C4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50353 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72.68;
74.68;
                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00430; HOLI;
                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     448 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID-10036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mesocricetus
                                 377;
 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lsoforms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                      Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8VHB7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART;
                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and
MYESVEVGGPTPNPFLVVDFYNQN-RACLLPEKGLPAPGPYSTPLRTPLWNGSN--HSIE 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
              EVGELIEKVRKAHQETFPALCQLGKYTTNNSSEQRVSLDIDLWDKFSELSTKCIIKTVEF
                                                                                                                                                                                                                           AKQLPGFTTLTIADQITLLKAACLDILILRICTRYTPEQDTMTFSDGLTLNRTQMHNAGF
                                                                                                                                                                                                                                                                                  GPLTDLVFAFANQLLPLEMDDAETGLLSAICLICGDRQDLEQPDRVDMLQEPLLEALKVY
                                                                                                                                                                                                                                                                                                                                           VRKRRPSRPHMFPKMLMKITDLRSISAKGAERVITLKMEIPGSMPPLIQEMLENSEGLDT
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Pfam: PF00105; zf-C4; 1.
ProDom; PD000035; znf_C4steroid; 1.
PROSITE; PS00031; NUCLEAR_RECEPTOR; UNKNOWN_1.
DNA-binding; Nuclear protein; Receptor; Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  448;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     448 AA; 50471 MW; BC8598A1D350701B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                   418 LSGQPGGGGRDGGGLPPPPGSCSPSLSPSSNRSSPATHSP 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1760; DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.1e-144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    448 AA
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L; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Coturnix coturnix (common quail).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Retinoic acid receptor beta-2. RAR-BETA-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72.28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 343; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=11133679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (01-DEC-2001 (01-JUN-2002 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zinc-finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Coturnix.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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SSPSPPPPPPRVYKPCFVCNDKSSGYHYGVSSCEGCKGFFRRSIQKNMVYTCHRDKNCIIN 135
                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00104; hormone_rec; 1.
Pfam; PF00105; zf-C4; 1.
                                                                                                                                                                                                -----GGGRDGGGLPPPP 436
                                                                                                                                                                                                                 454
                                                                                                                                                                                                                SSEDEAPGGQGKRGQSPQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
TISSUE-BREAST TUMOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zinc-finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                      Q91VK5;
                                                                                                                                                                                                                                                             Q91VK5
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                                                                                    117
                                                                             TCHRDKNCIINKVTRNPCQYCRLQKCFEVGMSKESVRNDRNKKKKEVPKPECSESYTLTP 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPPSPPPLPRIYKPCFVCQDKSSGYHYGVSACEGCKGFFRRSIQKNMYYTCHRDKNCIIN 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEKGLPAPG-PYSTP-----LRTPLWNG-----SNHSIETQSSSSEEIVP 68
              MYESVEVGCPTPNPFLVVDFYNQN-RACLLPEKGLPAPGPYSTPLRTPLW--NGSNHSIE
                                                                                                               EVGELIEKVRKAHQETFPALCQLGKYTTNNSSEQRVSLDIDLWDKFSELSTKCIIKTVEF
                                                                                                                                                  AKQLPGFTTLTIADQITLLKAACLDILILRICTRYTPEQDTMTFSDGLTLNRTQMHNAGF
                                                                                                                                                                                     GPLTDLVFAFANQLLPLEMDDAETGLLSAICLICGDRQDLEQPDRVDMLQEPLLEALKVY
                                                                                                                                                                                                                        VRKRRPSRPHMFPKMLMKITDLRSISAKGAERVITLKMEIPGSMPPLIQEMLENSEGLDT
                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA-binding; Nuclear protein; Receptor; Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                              32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    458;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  458 AA; 50917 MW; B410D52805BE7CDD CRC64;
                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Retinolc acid receptor, gamma.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                     418 LSGQPGGGGRDGGCLPPPPGSCSPSLSPSSNRSSPATHSP 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67.7%; Score 1651; DB 11;
72.2%; Pred. No. 9.1e-135;
ive 40; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00104; hormone_rec; 1.
Pfam; PF00105; zf-C4; 1.
ProDom; PD0000035; zf_C4ctorid; 1.
PROSITE; PS00031; NUCLEAR_RECEPTOR; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                         458 AA.
                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 317; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zinc-finger
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Q91YX2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 PGSGYPGAGFPFAFPGALRGSPPFEMLSPSFRGLGQPDLPKEMASLSVETQSTSSEEMVP 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30 PEKGLPAPG-PYSTP-----LRTPLWNG-----SNHSIETQSSSSEEIVP 68
KVTRNPCQYCRLQKCFEVGMSKESVRNDRNKKKKEVPKPECSESYTLTPEVGELIEKVRK
                   AHQETFPALCQLGKYTTNNSSEQRVSLDIDLWDKFSELSTKCIIKTVEFAKQLPGFTTLT
                                                                                               FPKMLMKITDLRSISAKGAERVITLKMEIPGSMPPLIQEMLENSEGLDTLSGQPG----
                                                                                                                                                      IADQITLLKAACLDILILRICTRYTPEQDTMTFSDGLTLNRTQMHNAGFGPLTDLVFAFA
                                                                                                                                                                                                                                NOLLPLEMDDAETGLLSAICLICGDRODLEOPDRVDMLOEPLLEALKVYVRKRRPSRPHM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Probom; PD000035; Znf_C4steroid; 1.
PROSITE; PS00031; NUCLEAR_RECEPTOR; UNKNOWN_1.
DNA-binding; Nuclear protein; Receptor; Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       458 AA; 50891 MW; 1D13D2F1482D7194 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67.7%; Score 1651; DB 11;
72.2%; Pred. No. 9.1e-135;
1ive 40; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         458 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence
01-UJVN-2002 (TrEMBLrel. 21, Last annotati
Similar to retinoic acid receptor, gamma.
Mus musculus (Mouse)
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----GGGRDGGGLPPP 435

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LEALKVYVRKRRPSRPHMFPKMLMKITDLRSISAKGAERVITLKMEIPGSMPPLIQEMLE 410
                                                                         QMHNAGFGPLTDLVFAFANQLLPLEMDDAETGLLSAICLICGDRQDLEQPDRVDMLQEPL 350
      IIKIVEFAKRLPGFTGLSIADQITLLKAACLDILMLRICTRYTPEQDTMTFSDGLTLNRT 286
                                                                                                                  411 NSEGLDTLSGQPG------
                                                                                                                                                                                                                                                      Plasmid aRARgamma2
                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                              NCBI_TaxID-8296;
                                                                                                                                                                                                                                                                                                                             TISSUE-EMBRYO,
                                                                                                                                                                                                                                                                                                                                                                                     development
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Matches 318;
                                                                                                                                                                                                                                                                                      Ambystoma
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                                                                                                                                                                                     Q918T3;
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                                                                            IADQITLLKAACLDILILRICTRYTPEQDTMTFSDGLTLNRTQMHNAGFGPLTDLVFAFA 308
                                                Sharma R.P., McGraw R.A., Dugyala R.R.;
"Cloning and characterization of hamster fetal retinoic acid receptor isoforms.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY046645; AAL02362.1;
InterPro; IPR000536; Hormone_rec_lig.
InterPro; IPR001723; Stdhrmn_receptor.
InterPro; IPR001628; Znf_C4steroid.
                                                                                                                   FPKMLMKITDLRSISAKGAERVITLKMEIPGSMPPLIQEMLENSEGLDTLSGQPG---- 423
                                                                                                                              112 QKNMVYTCHRDKNCIINKVTRNPCQYCRLQKCFEVGMSKESVRNDRNKKKKEVPKPECS- 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           171 ESYTLTPEVGELIEKVRKAHQETFPALCQLGKYTTNNSSEQRVSLDIDLWDKFSELSTKC 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 231 IIKTVEFAKQLPGFTTLTIADQITLLKAACLDILILRICTRYTPEQDTMTFSDGLTLNRT 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Retinoic acid receptor gamma-2.
Mesocricetus auratus (Golden hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 11; Length 443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67.6%; Score 1646.5; DB 11; Lengt 79.3%; Pred. No. 2.1e-134; 1ve 32; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 443 AA; 49431 MW; 36D86F26CBC4AB49 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00031; NUCLEAR_RECEPTOR; UNKNOWN_1
                                                                                                                                                                                                                                  443 AA
                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00104; hormone_rec; 1.
Pfam; PF00105; zf-C4; 1.
PRINTS; PR001398; STRDHORMONER.
PRINTS; PR00047; STROIDEINGER.
ProDom; PD000035; Znf_C4steroid; 1.
SMART; SM00430; HOLI; 1.
SMART; SM00399; ZnF_C4; 1.
                                                                                                                                                          -----GGGRDGGGLPPPP 436
                                                                                                                                                                              SSEDEAPGGQGKRGQSPQP 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 79.3
Matches 314; Conservative
                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                               NCBI_TaxID-10036;
                                                                                                                                                                                                                                                                                                                       Mesocricetus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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Q8VHB6
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57 ETQSSSSEEIVPSPPSPPPLPRIYKPCFVCQDKSSGYHYGVSACEGCKGFFRRSIQKNMV 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wirtanen L., Seguin C., "Cloning of cDNAs encoding retinoic acid receptors RARgammal, RARgamma2, and a new splicing variant, RARgamma3, from Ambystoma mexicanum and characterization of their expression during early
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochim. Biophys. Acta 1492:81-93(2000).

-1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

-1- SIMILARIYY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.

EMBL; AF206315; AAP80975.1; -.

HSSP; P22932; 3LBD.

InterPro; IPR000536; Hormone_rec_lig.

InterPro; IPR001628; Stdhrmn_receptor.

InterPro; IPR01628; Znf_C4steroid.

Pfam; PF00104; hormone_rec; 1.
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                                                                                                                                                                                                                                                    Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleost
Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
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                                              01-007-2000 (TrEMBLrel. 15, Created)
01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-0TN-2002 (TrEMBLrel. 21, Last annotation update)
Retonoic acid receptor gamma 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS: PRO0398; STRDDENNORR.
PRINTS: PRO047; STROIDFINGER.
PROD000035; Inf__dsteroid; 1.
SMART: SMO0399; Inf__dsteroid; 1.
SMART: SMO0399; Inf__dsteroid; 1.
PROSITE; PSO0031; NUCLEAR RECEPTOR; 1.
PROSITE; PSO0031; NUCLEAR PROFITE; Plasmid; Receptor; Indiad; Nuclear protein; Plasmid; Receptor; SEQUENCE 441 AA; 49865 MW; 906E25E145CEEEEE C
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ive 37; Mismatches
  441
  PRT;
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                                                                                                                                                                                                  Ambystoma mexicanum (Axolot1).
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PRELIMINARY;
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                                                                                                                                              FGPLTDLVFAFANQLLPLEMDDAETGLLSAICLICGDRQDLEQPDRVDMLQEPILLEALKV 356
                                                                                                                                                                                                                                                                 YVRKRRPSRPHMFPKMLMKITDLRSISAKGAERVITLKMEIPGSMPPLIQEMLENSEGL- 415
                                                 113 YTCHRDKNCQINKVTRNRCQYCRLQKCFEVGMSKEAVRNDRNKKKKEIKEEVVTDSYEMP 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                plasmid aRARgamma2I.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wirtanen L., Seguin C.;
"Cloning of cDNAs encoding retinoic acid receptors RARgammal,
RARgamma2, and a new solicing variant, RARgamma3, from Ambystoma
mexicanum and characterization of their expression during early
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biochim. Biophys. Acta 1492:81-93(2000).
-!-SIMILARITY).
-!-SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
-!-SIMILARITY: BELONGS 1.1;
-!-SIMILARITY: ARRONGS 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transcription regulation; Zinc-finger.
SEQUENCE 446 AA; 50277 MW; ZE552050A170EC28 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66.8%; Score 1628.5; DB 1:
74.0%; Pred. No. 7.9e-133;
ive 37; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS, PR00398; STRDHORMONER.
PRINTS, PR00047; STROIDFINGER.
PRODOM; PD000035; Znf_C4steroid; 1.
SMART; SM00439; ZnF_C4; 1.
PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
DNA-binding; Nuclear protein; Plasmid; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-2000 (TrEMBLrel. 15, Created) 01-0CT-2000 (TrEMBLrel. 15, Last sequ 01-JUN-2002 (TrEMBLrel. 21, Last ann Retonoic acid receptor gamma 21.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ambystoma mexicanum (Axolotl).
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tches 318; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                -DTLS 419
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Q918T2
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MYESVEVGGPTPNPFLVVDFYNQNRACLLPEKGL-PAPG---PYSTPLRTPLWNGSNHSI 56

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231
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                                                              YTCHRDKNCIINKVTRNPCQYCRLQKCFEVGMSKE----SVRNDRNKKKKEVPKPECSE 171
52
                                                                           SYTLIPEVGELIEKVRKAHQETFPALCQLGKYTTNNSSEQRVSLDIDLMDKFSELSTKCI
                                                                                                                                                                                              MHNAGFGPLTDLVFAFANQLLPLEMDDAETGLLSAICLICGDRQDLEQPDRVDMLQEPLL
1 MYDCMEAFMLAPHP--LYDVTNPG-ACMLRKARLSPCFGGLDPFGWPQPASL----QSV
                                                                                                                                                                                                                                                                                         SEGL--DILS 419
                                                                                                                                                                                                                                                                                                              413 PEAFEDDALS
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Search completed: March 29, 2003, 07:57:21 Job time : 65 secs

us-09-691-220-2.rsp

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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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- protein search, using sw model OM protein March 29, 2003, 05:12:23 ; Search time 23 Seconds
 (without alignments)
 824.117 Million cell updates/sec Run on:

US-09-691-220-2 2437

1 MYESVEVGGPTPNPFLVVDF.....SCSPSLSPSSNRSSPATHSP 457 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters:

112892 seqs, 41476328 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	P10276 homo sapien	P11416 mus musculu	Q90966 gallus gall		P51126 xenopus lae			mus m	Q9w6b3 coturnix co		a		P22932 homo sapien	P18911 mus musculu	_		P18516 notophthalm		P18515 notophthalm		P15204 xenopus lae		'n	Q28570 ovis aries	Q9w6n4 hippoglossu	7	_	Q91241 paralichthy	PO4625 gallus gall	Q02965 rana catesb		9 paralich	P18117 xenopus lae
SUMMAKIES		√	RRA_HUMAN	RRA_MOUSE /	RRA_CHICK (RRA_NOTVI	RRA_XENLA	RRA_FUGRU	RRB_HUMAN	RRB_MOUSE	RRB_COTJA	RRB_CHICK	RRG_BRARE	RRG1_HUMAN	RRG2_HUMAN	RRG1_MOUSE	RRG2_MOUSE	RRG2_XENLA	RRG_NOTVI	RRG1_XENLA	RRB_NOTVI	THA1_BRARE	THAA_XENLA	THAB_XENLA	THA_SALSA	THA1_SHEEP	THA_HIPHI	THA_RANCA	THAB_PAROL	THAA_PAROL	THA_CHICK	THB_RANCA	THA_CAIMO	THB_PAROL	THBA_XENLA
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	,	Length	462	462	460	458	458	447	455	482	455	455	499	454	443	458	447	442	502	476	158	427	418	418	416	410	416	418	391	416	408	373	401	395	373
de	Query	Match	87.3	85.7	82.9	80.9	77.8	76.7	72.3	72.0	71.2	71.1	68.3	٠	67.9	67.4	67.0	8.99	66.5	66.5	29.7	27.8	27.1	27.0	27.0	26.8	26.5	26.5	26.5	26.5	26.5	26.2	26.0	25.9	25.9
		Score	2127	2089	2020.5	1972	1895	1868.5	1761	1753.5	1736	1733	1663.5	1662	1655.5	1642	1633.5	1627.5	1621	1620.5	724	676.5	659.5	658	657.5	653	647	647	646.5	646	645.5	639		630.5	630
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5 aptenodytes 4 brachydanio	4 mus musculu 9 xenopus lae	8 homo sapien 6 rattus norv	2 gallus gall	3 nomo sapien 2 mus musculu	3 rattus norv	0 pygoscelis	3 avian eryth
042295 09pve4	P3724-	P1082	P1811	P3724	P1811:	04245	P0337
THA_APTPA THB_BRARE	THB2_MOUSE THBB_XENLA	THB1_HUMAN	THB_CHICK	THB2_HUMAN THB1_MOUSE	THB1_RAT	THA_PYGAD	ERBA_AVIER
			, ·		-	H	Н
402	475	461	369	476	461	402	385
25.8	25.7	25.5	25.4	25.3	25.2	24.9	24.9
629.5	625.5 625	622.5	618	617 615	615	607.5	606.5
34 35	36 37	38	40	412	43	44	45

ALIGNMENTS

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MEDLINE-91088249; PubMed-2175878;
Brand N.J., Petkovich M., Chambon P.;
Characterization of a functional promoter for the human retinoic acid
receptor-alpha (NRNR-alpha).
Nucleic Acids Res. 18:6799-6806(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 31-462 FROM N.A.
MEDLINE-88065872; PubMed-2825025;
Petkovich M., Brand N.J., Krust A., Chambon P.;
"A human retinoic acid receptor which belongs to the family of nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEGUENCE FROM N.A. (ISOFORM ALPHA-1).
MEDLINE-9926925; PubMed-10337631;
Hjalt T.A.H., Murray J.C.;
"Genomic structure of the human retinoic acid receptor-alphal gene.";
Mamm. Genome 10:528-529(1999).
                                                                                                                                                                                                                                                                                                                              MEDLINE=94134721; PubMed=8302850; Chen Z., Guidez F.O., Wang Z.-Y., Chen Z., Guidez F., Rousselot P., Agadir A., Chen S.-J., Wang Z.-Y., Degoso L., Zelent A., Waxman S., Chomienne C.; PLEF-RAR alpha fusion proteins generated from the variant t(11;17)(q23;q21) translocation in acute promyelocytic leukemia inhibit ligand-dependent transactivation of wild-type retinoic acid
RRA_HUMAN STANDARD; PRT; 462 AA.
P10276; Q13440; Q13441: P78456; Q9NQSO;
P10AR-1989 (Rel. 10, Created)
01-0CT-1989 (Rel. 11, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Retinoic acid receptor alpha (RAR-alpha).
RARA OR NRIB1.
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM ALPHA-1).
MEDLINE-88065922; PubMed=2825036;
Gluere V., Ong E.S., Segui P., Evans R.M.;
"Identification of a receptor for the morphogen retinoic acid.";
Nature 330:624-629(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 91:1178-1182(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-80 FROM N.A. (ISOFORM ALPHA-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM ALPHA-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 330:444-450(1987).
                                                                                                                                                                                       NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  receptors
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                                                                                                                                                                                                                                                                                                                                                                                                       ALTERNATIVE PRODUCTS: 2 ISOFORMS; ALPHA-1 (SHOWN HERE) AND ALPHA-2; ARE PRODUCED BY ALTERNATIVE SPLICING. THEY DIFFER ONLY IN THEIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN, A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN. DISEASE: FORMS OF ACUTE PRONYELOCYTIC LEUREMIA (APL) ARE CHARACTERIZED BY CHROMOSOMAL TRANSLOCATIONS T(11;17) (032:021) WHICH INVOLVES RARA AND PLZF, T(15;17) (021;021) WHICH INVOLVES SARA AND PLZF, T(15;17) (021;021) WHICH INVOLVES SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY. NRI SUBFAMILY:
                                                                                                                                                                                                                           Chen A., Petrie K., Waxman S., Zelent A.;
"Homo sapiens retinoic acid receptor alpha (RAR-alpha) gene, promoter and 5' region of RAR-alpha 2 isoform."
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
-! FUNCTION: THIS IS A RECEPTOR FOR RETINOIC ACID. THIS METABOLITE HAS PROPOUND EFFECTS ON VERTEBRATE DEVELOPMENT. RETINOIC ACID IS A MORPHOGEN AND IS A POWERFUL TERATOGEN. THIS RECEPTOR CONTROLS CELLS FUNCTIONS BY DIRECTLY REGULATING GENE EXPRESSION.
                                                                                           MEDLINE-96151966; PubMed-8562957; Redner R.L., Rush E.A., Faas S., Rudert W.A., Corey S.J.; Redner "The t(5:17) variant of acute promyelocytic leukemia expresses nucleophosmin_retinoic acid receptor fusion.";
       Chambon P.;
Submitted (DEC-1988) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                             SEQUENCE OF 1-54 FROM N.A. (ISOFORM ALPHA-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000536; Hormone_rec_lig.
InterPro; IPR001723; Stdhrmn_receptor.
InterPro; IPR001628; Znf_C4steroid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, AF088895, AAD05222.1; EMBL, AF0888995, AAD05222.1; FEMBL, AF0888991, AAD05222.1; JOINED. EMBL, AF088891, AAD05222.1; JOINED. EMBL, AF088892, AAD05222.1; JOINED. EMBL, AF088893, AAD05222.1; JOINED. EMBL, AF088894, AAD05222.1; JOINED. EMBL, X56685, CAA39533.1; JOINED. EMBL, X58685, CAA41532.1; JOINED. EMBL, X58685, CAA41532.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS, PRO0398; STRDHORMONER.
PRINTS; PRO0047; STROIDFINGER.
PRODOM; PD000035; Znf_C4steroid; 1.
SWART; SM00430; HOLL; 1.
SWART; SM00399; ZnF_C4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 U41742; AABO0112.1; ALT_INIT.
U41743; AABO0113.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Nuclear ALTERNATIVE PRODUCTS: 2 ISOFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00104; hormone_rec; 1.
Pfam; PF00105; zf-C4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X06614; CAA29829.1; -. EMBL; X06538; CAA29787.1; -.
                                                       SEQUENCE OF 61-462 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AF283809; AAF87249.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SM00430; HOLI; 1.
SM00399; ZnF_C4; 1.
                                                                                                                                                                         Blood 87:882-886(1996).
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TRANSFAC; T00719; -
Genew; HGNC:9864; RARA.
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PIR; S07272; S07272.
                                                                             TISSUE-Bone marrow;
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MASNSSSCPTPGGGHLNGYPVPPYAFFFPPMLGGLSPPGAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    251
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                                                                                                                                                                                                                                                                                                                                                            67 VPSPPSPPPLPRIYKPCFVCQDKSSGYHYGVSACEGCKGFFRRSIQKNMVYTCHRDKNCI 126
                                                                                                                                                                                                                                                                                                                                                                         Gaps
PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
Receptor; Transcription regulation; DNA-binding; Nuclear protein; Cinc-finger; Multipene family; Alternative splicing; Proto-oncogene; Chromosomal translocation and MODULATING.
DOWALIN 8 153 NUCLEAR RECEPTOR-TYPE.
ZN_FING 88 108 C4-TYPE.
ZN_FING 124 148 C4-TYPE.
DOMAIN 154 199 HINGE.
DOMAIN 200 419 LIGAND-BINDING.
                                                                                                                                                                                                                                                                                                          7 VGGPTPNPFLVVDFYNQNRACLLPEKGLPAPGPYSTPLRTPLWNGSNHSIETQSSSSEEI 66
                                                                                                                                                                                                                                                                                                                                   32 LGGLSP-PGALTTLQHQ------LPVSG-YSTP-----SPATIETQSSSSEEI 71
                                                                                                                                                                                                                                                                                                                                                                                                                        BREAKPOINT FOR TRANSLOCATION TO FORM PLZF-RAR-ALPHA AND RAR-ALPHA1-PLZF
                                                                                                                                                                                                                                                                                                                                                                                                                                                            RKAHQETFPALCQLGKYTTNNSSEQRVSLDIDLWDKFSELSTKCIIKTVEFAKQLPGFTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LTIADQITLLKAACLDILILRICTRYTPEQDTMTFSDGLTLNRTQMHNAGFGPLTDLVFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FANQLLPLEMDDAETGLLSAICLICGDRQDLEQPDRVDMLQEPLLEALKVYVRKRRPSRP
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                 20;
                                                                                                                                                                                                                                                        Length 462;
                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                  -> D (IN REF. 3).
E8D1CF9A1E57CB99 CRC64;
                                                                                                                                                                                                                                                       Score 2127; DB 1;
Pred. No. 2.5e-149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RRA MOUSE STANDARD; PRT; 462 AA. P11416; P22603; 01-0CT-1989 (Rel. 12, Created) 01-0CT-1989 (Rel. 12, Last sequence update) 15-JUM-2002 (Rel. 41, Last annotation update) Retinoic acid receptor alpha (RAR-alpha). Mus musculus (Mouse).
                                                                                                                                                                                                     ISOFORM ALPHA-2)
                                                                                                                                                                                                                                          87.3%; SCor.
9 91.6%; Pred. No. 4...
5; Mismatches
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MEDLINE-89295563; PubMed-2544807;
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50771 MW;
                                                                                                                                                                                                                                                                                 Matches 413; Conservative
                                                              153
108
148
199
419
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462 AA;
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88
124
200
60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDINE-FROM N.A. (VARIANT IN EMBRYONAL CARCINOMA CELL LINE RAC65).

MEDINE-91061752; Pubbed-2174108;
Pratt M.A.C., Kralova J., McBurney N.W.;
The second of the alpha retinoic acid receptor T. McCall Biol. 10:645-643(1990).

10. Cell. Biol. 10:645-643(1990).

11. FUNCTION: THIS IS A RECEPTOR FOR RETINOIC ACID IS HAS PROFOUND EFFECTS ON VERTEBRATE DEVELOPMENT. RETINOIC ACID IS CELLS FUNCTIONS BY DIRECTLY REGULATING GENE EXPRESSION.

11. AUTRINOIC DOCATION: Nuclear.

12. ARE PRODUCED BY ALTERNATYE SPLICING.

23. ARE PRODUCED BY ALTERNATYE SPLICING.

24. ADDAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN, ADDAINS BEINDING DOMAIN, AND A C-TERMINAL STEROID-BINDING DOMAIN.

25. ALBERDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.

26. INTI SUBFAMILY:

27. ALBERDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
Zelent A., Krust A., Petkovitch M., Kastner P., Chambon P.; "Cloning of murine alpha and beta retinoic acid receptors and a novel receptor gamma predominantly expressed in skin."; Nature 339:714-717(1989).
                                                                                                                                                Helermann R., Rentrop M., Lang E., Maelicke A.; "Cloning of several genes coding for retinoic acid nuclear receptors in the mouse embryonal carcinoma cell line PCC7-MZ1."; J. Recept. Res. 13:693-709(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (VARIANT IN EMBRYONAL CARCINOMA CELL LINE RAC65). MEDLINE-92324516; PubMed-1320576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kruyt F.A.E., van der Veer L., Mader S., van den Brink C.E., Feijen A., Jonk L.J., Kruijer W., van der Saag P.T.; "Retinoic acid resistance of the variant embryonal carcinoma cell
                                                                                                                                                                                                                                                                                                           Leroy P., Krust A., Zelent A., Mendelsohn C., Garnier J.-M., Astrar P. Dieritch A., Chambon P.;
"Multiple isoforms of the mouse retinoic acid receptor alpha are generated by alternative splicing and differential induction by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           line RAC65 is caused by expression of a truncated RAR alpha."; Differentiation 49:27-37(1992).
                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORMS ALPHA-1 AND ALPHA-2).
MEDLINE-91114713; PubMed-1846598;
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InterPro; IPR001723; Stdhrmn_receptor.
InterPro; IPR001628; Znf_C4steroid.
                                                                                                           SEQUENCE FROM N.A. (ISOFORM ALPHA-1).
MEDLINE-93195858; PubMed-8383767;
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EMBL; X56565; CAA39917.1; -.
EMBL; X56656; AAB2578.1; -.
EMBL; X57528; CAA40749.1; -.
EMBL; M60909; AAA40031.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S05050; S05050.
S13599; S13599.
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TRANSFAC; T01336; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P10826; 1HRA.
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                                                                                                                                                                                                                                                                                                                                                                                                retinoic acid.
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(IN ISOFORM ALPHA-2).

G -> A (IN EMBRYONAL CARCINOMA CELL LINE MARSES).

MISSING (IN EMBRYONAL CARCINOMA CELL LINE RAC65).
                                                                                                                                                     MASNSSSCPTPGGGHLNGYPVPPYAFFFPPMLGGLSPPGAL
TSLQHQLPVSGYSTPSPAT -> MYESVEVGGLTPAPNPFL
VVDFYNQNRACLLQEKGLPAPGPYSTPLRTPLWNGSNHS
                                                                                                                                                                                                                                                                                                                                                                                                                                127 INKVTRNPCQYCRLQKCFEVGMSKESVRNDRNKKKKEVPKPECSESYTLTPEVGELIEKV 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LTIADQITLLKAACLDILILRICTRYTPEQDTMTFSDGLTLNRTQMHNAGFGPLTDLVFA 306
                                                                                                                                                                                                                                                                                                                                                                                     67 VPSPPSPPPLPRIYKPCFVCQDKSSGYHYGVSACEGCKGFFRRSIQKNMVYTCHRDKNCI 126
                                                                                                                                                                                                                                                                                                                                                                                                 HMFPKMLMKITDLRSISAKGAERVITLKMEIPGSMPPLIQEMLENSEGLDTLSGQPGGGG 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32 LGGLSP-PGALTSLQHQ------LPVSG-YSTP-----SPATIETQSSSSEEI 71
                                                                                                                                                                                                                                                                                                                     20; Gaps
                                                                                                                                                                                                                                                                                                                                           7 VGGPTPNPFLVVDFYNQNRACLLPEKGLPAPGPYSTPLRTPLWNGSNHSIETQSSSSEEI 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RKAHQETFPALCQLGKYTTNNSSEQRVSLDIDLWDKFSELSTKCIIKTVEFAKQLPGFTT
         PRINTS; PRO0047; STROIDFINGER.

SMART; SM00430; LDE_C4steroid; 1.

SMART; SM00399; ZnF_C4; 1.

SMART; SM00399; ZnF_C4; 1.

SMOSITE; S00031; NUCLEAR_EXERPTOR; 1.

Receptor; Transcription requiation; DNA-binding; Nuclear protein; Zinc-finger; Multigene family; Alternative splicing.
                                                                                                                                                                                                                                                                                              Length 462;
                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                         726F7799633A85AD CRC64;
                                                                                               NUCLEAR RECEPTOR-TYPE. C4-TYPE.
                                                                                                                                                                                                                                      -> K (IN REF. 5).
-> S (IN REF. 5).
-> L (IN REF. 5).
                                                                                                                                                                                                                                                                                             Score 2089; DB 1;
Pred. No. 1.6e-146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RRA_CHICK STANDARD; PRT; 460 AA. 090966; 09097; 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) RARA OR NRIB1.
                                                                                                                                          LIGAND-BINDING
                                                                                                                                                                                                                                                                                                                    8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RDGGGLPPPPGSCSPSLSPSSNRSSPATHSP 457
                                                                                       MODULATING
                                                                                                                     C4-TYPE.
                                                                                                                               HINGE
PRINTS; PR00398; STRDHORMONER.
PRINTS; PR00047; STROIDFINGER.
                                                                                                                                                                                                                                                                          50735 MW;
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90.0%;
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179
284
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179
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462 AA;
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124
154
200
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                                                                                                                                                                                                                                                                                                                     Matches 406;
                                                                                               DNA_BIND
ZN_FING
ZN_FING
DOMAIN
DOMAIN
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RRA_CHICK
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NCBI_TaxID=8316;
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                                                                                          Michaille J.J., Kanzler B., Blanchet S., Garnier J.M., Dhouailly D.;

"Characterization of cDNAs encoding two chick retinoic acid receptor
alpha isoforms and distribution of retinoic acid receptor alpha, beta
and gamma transcripts during chick skin development.";

Int. J. Dev. Biol. 39:587-596(1995).

- FUNCTION: THIS IS A RECEPTOR FOR RETINOIC ACID. THIS METABOLITE
AS PROFOUND EFFECTS ON VERTEBRATE DEVELOPMENT. RETINOIC ACID IS
A MORPHOGEN AND IS A POWERED. TERATOGEN. THIS RECEPTOR CONTROLS
CELLS FUNCTIONS BY DIRECTLY REGULATING GENE EXPRESSION.

- SUBJECT OF ALTERNATIVE PRODUCTS: 2 ISOFORMS; ALPHA-1 (SHOWN HERE) AND ALPHA-

- I- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN.

- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN.

- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.

- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIGAND-BINDING.
MASNSSSCPTPGGGHLNGYPVTPYAFFFPHMLGGLSPPSSLPGIQHQLPVSGYSTPSPAT -> MFEGAEVAGLPPPGPLPRMDCGGPGRGCLLPQCPPPFTAPRRAPHWGASGRS (IN
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galllformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYGVSACEGCKGFFRRSIQKNMVYTCHRDKNCIINKVTRNPCQYCRLQKCFEVGMSKESV 153
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Receptor; Transcription regulation; DNA-binding; Nuclear protein; Zinc-finger; Multigene family; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LPAPGPYSTPLRTPLWNGSNHSIETQSSSSEEIVPSPPSPPPLPRIYKPCFVCQDKSSGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Pred. No. 1.7e-141;
10; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99711F415E811CA2 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro: IPR000536; Hormone_rec_lig.
InterPro: IPR001723; Stdhrmn_receptor.
InterPro: IPR001628; Znf_C4steroid.
Pfam; PF00104; hormone_rec; 2.
Pfam; PF00105; zf-C4; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C4 - TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PRO0398; STRDHORMONER.
PRINTS; PRO0047; STROIDFINGER.
PRODOM; PD000035; Enf_c4steroid; 1.
SMART; SM00430; HOLI; 1.
SMART; SM00399; ZnF_C4; 1.
                                                                      SEQUENCE FROM N.A. MEDLINE-96192630; PubMed-8619957;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MW.
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91.5%;
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388; Conservative
 Gallus gallus (Chicken)
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108
148
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419
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                                               NCBI_TaxID=9031;
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ZN_FING
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VARSPLIC
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MEDLINE-90015190; PubMed-2552324;
Ragsdale C.W. Jr., Petkovich M., Gates P.B., Chambon P., Brockes J.P.,
"Identification of a novel retinoic acid receptor in regenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDINE-93087213; PubMed=1333589;
Ragsdale C.W., Gates P.B., Brockes J.P.;
"Identification and-expression pattern of a second isoform of the newt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: Nuclear.
-!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; ALPHA-1 (SHOWN HERE) AND ALPHA-2; ARE PRODUCED BY ALTERNATIVE SPLICING.
-!- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN, A DATA BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
-!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
                                   218
                                                                                                                                                                                                                                                                                                         RQDLEQPDRVDMLQEPLLEALKVYVRKRRPSRPHMFPKMLMKITDLRSISAKGAERVITL 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KMEIPGSMPPLIQEMLENSEGLDTLSGQPGGGRDGGGLPPPPGSCSPSLSPSSNRSSPA 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alpha retinoic acid receptor.";
Nucleic Acids Res. 20:5811-5811(1992).
-!- FUNCTION: THIS IS A RECEPTOR FOR RETINOIC ACID. THIS METABOLITE
HAS PROFOUND EFFECTS ON VERTEBRATE DEVELOPMENT. RETINOIC ACID IS
A MORPHOGEN AND IS A POWERFUL TERATOGEN. THIS RECEPTOR CONTROLS
CELLS FUNCTIONS BY DIRECTLY REGULATING GENE EXPRESSION.
                                                                                                                                                  SLDIDLWDKFSELSTKCIIKTVEFAKQLPGFTTLTIADQITLLKAACLDILILRICTRYT
                                                                                                                                                                                                                                                                      PEQDTMTFSDGLTLNRTQMHNAGFGPLTDLVFAFANQLLPLEMDDAETGLLSAICLICGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Notophthalmus viridescens (Eastern newt) (Triturus viridescens). Estaryota: Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Notophthalmus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RRA_NOTVI STANDARD; PRT; 458 AA. P18514; 091155; 01-NOV-1990 (Rel. 16, Created) 1-NOV-1990 (Rel. 16, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Retinoic acid receptor alpha (RAR-alpha)
RARA OR NR1B1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tissues of the newt.";
Nature 341:654-657(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NR1 SUBFAMILY
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Retinoic acid receptor alpha (RAR-alpha).
              RARA OR NR1B1.
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SEQUENCE
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                                                                                                                                                                                     MASNGGSCPSSGGHNNGYPVPHYAFFFPHMLGGLSPPGSLA
GIPHPLPVSAYSTPSPAT -> MYDSVEVSSPSPYIMIDFY
SQNRACLMADKGLGHPVPFGSPIRNPHWSSSSHS (IN
                                                                                                                                                                                                                                                                                                           SSGYHYGVSACEGCKGFFRRSIQKNMVYTCHRDKNCIINKVTRNPCQYCRLQKCFEVGMS 149
                                                                                                                                                                                                                                                                                                                                SEQRVSLDIDLWDKFSELSTKCIIKTVEFAKQLPGFTTLTIADQITLLKAACLDILILRI 268
                                                                                                                                                                                                                                                                                                                                                                                               329 LICGDRODLEQPDRVDMLQEPLLEALKVYVRKRRPSRPHMFPKMLMKITDLRSISAKGAE 388
                                                                                                                                                                                                                                                                                                                                                                                                                                       389 RVITLKMEIPGSMPPLIQEMLENSEGLDTLSGQPGGGRDGGGLPPPPGSCSPSLSPSSN 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                   33 GLPAPGP---YSTPLRTPLWNGSNHSIETQSSSSEEIVPSPPSPPPLPRIYKPCFVCQDK 89
                                                                                                                                                                                                                                                                             SMART; SM00430; HOLI; 1.
SMART; SM00439; ZnF_C4; 1.
PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
Receptor; Transcription regulation; DNA-binding; Nuclear protein; Zinc-finger; Multigene family; Alternative splicing.
                                                                                                                                                                                                                                                      18; Indels 16;
                                                                                                                                                                                                                                       Length 458;
                                                                                                                                                                                                                      B4370822FBAADB54 CRC64;
                                                                                                                                             NUCLEAR RECEPTOR-TYPE. C4-TYPE.
                                                                                                                                                                                                                                     80.9%; Score 1972; DB 1;
88.3%; Pred. No. 6.4e-138;
.ive 16; Mismatches 18;
                                                                                                                                                                                                               ISOFORM ALPHA-2)
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Last annotation update)
                                                                                                                                                                               LIGAND-BINDING.
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                                                                                                                                       MODULATING
                      HSSP; P10826; 1HRA.
InterPro; IRR000536; Hormone_rec_lig.
InterPro; IPR001723; Stdhrmn_receptor.
InterPro; IPR001828; Znf_C4steroid.
Pfam; PF00104; hormone_rec; 2.
Pfam; PF00105; zf_C4; 2.
                                                                                                                                                              C4 - TYPE.
                                                                    PRINTS, PRO0398; STRDHORMONER.
PRINTS; PRO0047; STROIDFINGER.
ProDom; PD000035; Znf_C4steroid; 1.
                                                                                                                                                                      HINGE
                                                                                                                                                                                                                      50637 MW;
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(Rel. 34, Last sequ
(Rel. 40, Last anno
                                                                                                                                                                                                                                             88.38;
 X17585; CAA35602.1;
Z14254; CAA78621.1;
                                                                                                                                                                                                                                            Best_Local Similarity 88.39
Matches 379; Conservative
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                                                                                                                                             152
                S06123.
                                                                                                                                                                                                                      458 AA;
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87
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01-OCT-1996 (
16-OCT-2001 (
                 806123
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P51126;
                                                                                                                                             DNA_BIND
ZN_FING
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DOMAIN
DOMAIN
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RRA_XENLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBCELLULAR LOCATION: NOLGER.
-!- SUBCELLULAR LOCATION: NOLGER.
-!- DEVELOPMENTAL STAGES: IT IS SYNTHESIZED DURING OOGENESIS AND PERSISTS IN THE CLEAVING EMBRYO AT APPROXIMATELY CONSTANT LEVELS.
-- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATION.
A DAM-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
-!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
-- NRI SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                 ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                            PUCC. Natl. Acad. Sci. U.S.A. 89:2321-2325(1992).
-!- FUNCTION: THIS IS A RECEPPOR FOR RETINOIC ACID. THIS METABOLITE
-!- FUNCTION: THIS IS A RECEPPOR FOR RETINOIC ACID.
-!- FOR SCHOOL FUNCTION OF SCIENCE ON VERTEBRATE DEVELORMENT. RETINOIC ACID IS
A MORPHOGEN AND IS A POWERFUL TERATOGEN. THIS RECEPTOR CONTROLS
CELLS FUNCTIONS BY DIRECTLY REGULATING GENE EXPRESSION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                      Blumberg B., Mangelsdorf D.J., Dyck J.A., Bittner D.A., Evans R.M., de Robertis E.M.;
                                                                                                                                                                                                                                                                                                                                       "Multiple retinoid-responsive receptors in a single cell: families retinoid 'X' receptors and retinoic acid receptors in the Xenopus
Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 PPPGPGHINGFHVPHYAFFFPHMLGGMSXTGGLPGVQHQPPLSGYSTP----SPAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77.8%; Score 1895; DB 1; Length 458; 80.5%; Pred. No. 3e-132; ive 20; Mismatches 44; Indels 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
Receptor; Transcription regulation; DNA-binding; Nuclear
Zinc-finger; Multigene family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEAR RECEPTOR-TYPE, C4-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR00535; -. InterPro; IPR00535; Stdhrmn_receptor. InterPro; IPR001723; Stdhrmn_receptor. InterPro; IPR001628; Znf_C4steroid. Pfam; PF00104; hormone_rec; 1. PR01104; hormone_rec; 1. PR01104; hormone_rec; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C4-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PRO0398; STRDHORMONER.
PRINTS; PRO0047; STROIDFINGER.
PRODOM; PD000035; Znf_C4steroid; 1.
SMART; SM00430; HOLI; 1.
SMART; SM00399; ZnF_C4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; L11445; -; NOT_ANNOTATED_CDS.
HSSP; P10826; 1HRA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HINGE
                                                                                                                                                                                                                                       MEDLINE-92196110; PubMed-1312717;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50573 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 80.5
Matches 372; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             153
108
148
199
                                                                                                                Xenopodinae; Xenopus.
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154
200
458 AA;
                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                        NCBI_TaxID-8355;
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ZN_FING
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us-09-691-220-2.rsp

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Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-99384012; PubMed-10452951;
A Wentworth J.M., Schoenfeld V., Meek S., Elgar G., Brenner S.,
Chatterjee K.K.;
Chatterjee K.K.;
Tsolation and characterization of the retinoic acid receptor-alpha
gene in the Japanese pufferfish, F. rubripes.";
Gene 236:315-323(1999).

-I- FUNCTION: THIS IS A RECEPTOR FOR RETINOIC ACID. THIS METABOLITE
HAS PROFOUND BEFECTS ON VERTEBRATE DEVELOPMENT. RETINOIC ACID IS
CELLS FUNCTIONS BY DIRECTLY REGULATING GENE EXPRESSION.

-I- SUBCELLULAR LOCATION: NACIEAR.

-I- ALTERNATIVE PRODUCTS: 2 ISOFORMS; ALPHA-1 (SHOWN HERE) AND ALPHA-
Z; ARE PRODUCED BY ALTERNATIVE SPLICING.

-I- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN.

A DAN-BINDING DOMAIN AND A C-PREMINAL STEROID-BINDING DOMAIN.

-I- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
                                                                                                                                                                                 235
                                                                                                                  296 GFGPLTDLVFAFANQLLPLEMDDAETGLLSAICLICGDRQDLEQPDRVDMLQEPLLEALK 355
                                                                                                                                                                                                                                                                                                   356 VYVRKRRPSRPHMFPKMLMKITDLRSISAKGAERVITLKMEIPGSMPPLIQEMLENSEGL 415
                                                                                                                                                                                                                                                                                                                                                                                                VYTCHRDKNCIINKVTRNPCQYCRLQKCFEVGMSKESVRNDRNKKKKEVPKPECSESYTL 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota: Metzoca; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthom
                                                                                         TPEVGELIEKVRKAHQETFPALCQLGKYTTNNSSEQRVSLDIDLWDKFSELSTKCIIKTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    416 DTLSGQPGGGRDGGLPPPPGSCSPSLSPSSNRSSPATHSP 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RARA OR NRIBI.
Fugu rubripes (Japanese pufferfish) (Takifugu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RRA_FUGRU STANDARD; PRT; 447 AA Q9W523; Q9W524; 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Retinoic acid receptor alpha (RAR-alpha).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, AJ012382; CAB96754.1; -.
EMBL, AJ012380; CAB96754.1; JOINED.
EMBL, AJ012381; CAB43979.1; -.
EMBL, AJ012380; CAB43979.1; JOINED.
EMBL, AJ012378; CAB43870.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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116
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MAGKGNPVPGPHLNGFPVPTYSYFFPHMLGSLSPPALPGLP
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RGCLIPEKGLVPGAPHPYSTSIRNOHWNGSNHS (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHRDKNCIINKVTRNPCQYCRLQKCFEVGMSKESVRNDRNKKKKEVPKPECSESYTLTPE 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QSSSSEEIVPSPPSPPPLPRIYKPCFVCQDKSSGYHYGVSACEGCKGFFRRSIQKNMVYT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 GGPTPNPFL-----VVDFYNQNRACLLPE--KGLPAPGPYSTPLRTPLWNGSNHSIET 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RRB_HUMAN STANDARD; PRT; 455 AA.
P10826; Q00989; Q15298; Q9IN48; P12891;
01-701-1989 (Rel. 11, Created)
115-JUN-2002 (Rel. 41, Last sequence update)
115-JUN-2002 (Rel. 41, Last sequence update)
Retinoic acid receptor beta (RAR-beta) (RAR-epsilon) (HBV-activated)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00430; HOLT; 1. SMART; SM00430; LAFC4; 1. PROSITE; PS000319; ZAFC4; 1. PROSITE; PS00031; NUCLEAR_ECEPTOR; 1. Receptor; Transcription regulation; DNA-binding; Nuclear protein; Zinc-finger; Multigene family; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RKRRPSRPHMFPKMLMKITDLRSISAKGAERVITLKMEIPGSMPPLIQEMLENSEGLDTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     179 VGELIEKVRKAHQETFPALCQLGKYTTNNSSEQRVSLDIDLWDKFSELSTKCIIKTVEFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLTDLVFAFANQLLPLEMDDAETGLLSAICLICGDRQDLEQPDRVDMLQEPLLEALKVYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  E00630F720B1508D CRC64;
                                                                                                                                                                                                                                                     NUCLEAR RECEPTOR-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1868.5; DB 1
Pred. No. 2.6e-130;
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                                                                                                                                                                                                                                                                                                                                                                                                     ISOFORM ALPHA-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIGAND-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25; Mismatches
                            InterPro; IPR000536; Hormone_rec_lig.
InterPro; IPR001628; Znf_C4steroid.
Pfam; PF00104; hormone_rec; 2.
Pfam; PF00105; zf-c4; 2.
                                                                                                                                                                                                                                                                                                            HINGE
                                                                                                      PRINTS; PR00047; STROIDFINGER.
ProDom; PD000035; Znf_C4steroid;
CAB43871.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                    447 AA; 49532 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      76.78;
79.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein).
RARB OR NR1B2 OR HAP.
                 HSSP; P10826; 1HRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                     80
80
116
146
192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 366;
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ZN_FING
DOMAIN
DOMAIN
VARSPLIC
                                                                                                                                                                                                                                                     DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      414
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ZN_FING
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                                 SOURCE STATE THE THE THE TENT TO SEE SOURCE 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Houle B., Pelletier M., Wu J., Goodyer C., Bradley W.E.;
"Fetal isoform of human retinoic acid receptor beta expressed in small
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-88189352; PubMed-2833708; Brand N., Petkovitch M., Krust A., Chambon P., de The H., Marchio A., Tiollais P., Dejean A.; Identification of a second human retinoic acid receptor."; Nature 332:850-853(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRUCTURE BY NMR OF 82-160.
MEDLINE-91192652; PubMed-8383553;
Knegtel R.M., Katahira M., Schilthuis J.G., Bonvin A.M., Boelens R.,
Elib D., van der Saag P.T., Kaptein R.;
"The solution structure of the human retinoic acid receptor-beta DNA-binding domain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-86257411; PubMed-3014347;
MEDLINE-86257411; PubMed-3014347;
Dejean A., Bougueleret L., Grzeschik K.-H., Tiollais P.;
"Hepatitis B virus DNA integration in a sequence homologous to verb-A and steroid receptor genes in a hepatocellular carcinoma.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -! - FUNCTION: THIS IS A RECEPTOR FOR RETINOIC ACID. THIS METABOLITE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-92338160; PubMed-1321662;
Kathira M., Knegtel R.M.A., Boelens R., Eib D., Schilthuis J.G., van der Saag P.T., Kaptein R.;
"Homo- and heteronuclear NMR studies of the human retinoic acid receptor beta DNA-binding domain: sequential assignments and identification of secondary structure elements.";
                                                                                                                                                                                                         MEDLINE-88232961; PubMed-2836738;
Benbrook D., Lernherdt E., Pfahl M.;
"A new retinoic acid receptor identified from a hepatocellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            de The H., Marchio A., Tiollais P., Dejean A.;
"A novel steroid thyroid hormone receptor-related gene
inappropriately expressed in human hepatocellular carcinoma.";
Nature 330:667-670(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Liver;
MEDLINE-91014673; PubMed-2170809;
Dejean A., de The H.;
"Hepatitis B virus as an insertional mutagene in a human hepatocellular carcinoma.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-72 FROM N.A. (ISOFORM BETA-1).
MEDLINE-94101604; Pubmed-8275470;
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM BETA-2).
MEDLINE-88065931; Pubmed=2825037;
                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM BETA-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM BETA-4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cancer Res. 54:365-369(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 61-109 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                            Nature 333:669-672(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cell lung cancer lines.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 322:70-72(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Breast tumor;
                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                     TISSUE-Placenta;
                                                                                                                                                                                                                                                                                                                     carcinoma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001536; Hormone_rec_lig.
R InterPro; IPR001523; Stdhrmn_receptor.
R InterPro; IPR001628; Znf__dsteroid.
R InterPro; IPR001628; Znf__dsteroid.
R Pfam; PF00104; hormone_rec; 2.
R Pfam; PF00105; Zf-C4; 4.
R PRINTS; PR00199; STRDIDFINGER.
R PRINTS; PR00199; STR_C4steroid; 1.
R PRINTS; PR0019035; Znf__C4steroid; 1.
R PRO01TE; S000031; Znf__C4steroid; 1.
R PRO01TE; PS000031; NuCLEAR, RECEPTOR; 1.
R PRO01TE; PS000031; NuCLEAR, RECEPTOR; 1.
R PRO01TE; PS000031; NuClear, PS00031; Nuclear protein; Nu Zinc-finger; Multigene family; Alternative splicing; Proto-oncogene;
HAS PROPOUND EFFECTS ON VERTEBRATE DEVELOPMENT. RETINOIC ACID IS A MORPHOGEN AND IS A POWERFUL TERATOGEN. THIS RECEPTOR CONTROLS CELLS FUNCTIONS BY DIRECTLY REGULATING GENE EXPRESSION.

-!- SUBCELLULAR LOCATION: Nuclear (isoforms beta-1 and beta-2) and cytoplasmic (isoform beta-4).

-!- ALTERNATIVE PRODOUTS: 4 isoforms; beta-1 (shown here), beta-2, beta-3 and beta-4; are produced by alternative splicing.

-!- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN, A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINING DOMAIN.

-!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.

NR1 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIGAND-BINDING.
MTTSGHACPVPAVNGHMTHYPATPYPLLFPPVIGGLSLPPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HGLHGHPPPSGCSTPSPAT -> MFDCMDVLSVSPGQILDF
YTASPSSCMLQEKALKACFSGLTQTEWQHRHTAQS (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ISOFORM BETA-2).

MISSING (IN ISOFORM BETA-4).

G -> A (IN REF. 2).

L -> Q (IN REF. 1).

L -> M (IN REF. 1).

V -> L (IN REF. 1).
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C4-TYPE.
C4-TYPE.
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EMBL, X77664; CAA54740.1; --
EMBL, X04014; CAA5773.1; ALT_SEQ.
EMBL, M57445; AAA58728.1; --
P.R.; S02827; S02827.
PIR; A29492; A29492.
PIR; A2971; TVHUEA.
PIR; A25721; TVHUEA.
PIR; A25721; TVHUEA.
TRANSFAC; T00721; --
TRANSFAC; T01326; --
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MIM; 180220; -.
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455 AA;
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ZN_FING
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                                                                                                                                                         LKMEIPGSMPPLIQEMLENSEGLDTLSGQPGGGRDGGGLPPPPGSCSPSLSPSSNRSSP 452
                                                                                                                                                                                                                               Zelent A., Krust A., Petkovitch M., Kastner P., Chambon P.; "Cloning of murine alpha and beta retinoic acid receptors and a novel receptor gamma predominantly expressed in skin."; Nature 339:714-717(1989).
                         97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Heiermann R., Rentrop M., Lang E., Maelicke A.; "Cloning of several genes coding for retinoic acid nuclear receptors in the mouse embryonal carcinoma cell line PCC7-MZ1."; J. Recept. Res. 13:693-709(1993).
             VRNDRNKKKKEVPKPECSESYTLTPEVGELIEKVRKAHQETFPALCQLGKYTTNNSSEQR
                                                                                                                      GLPAPGPYSTPLRTPLWNGSNHSIETQSSSSEEIVPSPPSPPPLPRIYKPCFVCQDKSSG
                                       93 YHYGVSACEGCKGFFRRSIQKNMVYTCHRDKNCIINKVTRNPCQYCRLQKCFEVGMSKES
                                                                                                             VSLDIDLWDKFSELSTKCIIKTVEFAKQLPGFTTLTIADQITLLKAACLDILLLRICTRY
                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 receptor beta generated by usage of two promoters and alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zelent A., Mendelsohn C., Kastner P., Krust A., Garnier J.-M.,
Ruffenach F., Leroy P., Chambon P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Differentially expressed isoforms of the mouse retinoic acid
                                                                                                                                                                                                                                                                                                                                                                                                                       [1]
SEQUENCE FROM N.A. (ISOFORMS BETA-1; BETA-2 AND BETA-3).
                                                                                                                                                                                                                                                                                                                    RRB_MOUSE STANDARD; PRT; 482 AA. P22605; P22604; P11417; 01-00T-1989 (Rel. 12, Created) 1-00T-1989 (Rel. 19, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Retinolc acid receptor beta (RAR-beta).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM BETA-2).
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MEDLINE-93195858; PubMed-8383767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [4]
SEQUENCE FROM N.A. (ISOFORM BETA-4).
                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=C57BL/C;
MEDLINE=91114714; PubMed=1846599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-89295563; PubMed-2544807;
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                                                                                                                                                                                                                                                                                                                                                                                   musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID-10090;
                                                                                                                                                                                                                                                          ATHSP 457
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Mus musculus (
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                                                                                                             PICC. NATI. Acad. Sci. U.S.A. 89:2718-2722(1992).

-I FUNCTION: THIS IS A RECEPTOR FOR RETINOIC ACID. THIS METABOLITE HAS PROFOUND EFFECTS ON VERTEBRATE DEVELOPMENT. RETINOIC ACID IS A MORPHOGEN AND IS A POWERFUL TERATOGEN. THIS RECEPTOR CONTROLS CELLS FUNCTIONS BY DIRECTLY REGULATING GENE EXPRESSION.
-! SUBCELLULAR LOCATION: NUCLEAR.
-! ALTERNATIVE PRODUCTS: 4 ISOFORMS; BETA-1, BETA-2, BETA-3 (SHOWN HERE) AND BETA-4; ARE PRODUCED BY ALTERNATIVE SPLICING.
-! DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN, A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
-! SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
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HGLHGHPPPSGCSTPSPASVGQACQRTTGGSQFAASTKWTP
SLNAA -> MFDCMDVLSVSPGQILDFYTASPSSCMLQEKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00011, NUCLEAR RECEPTOR; 1.
Receptor; Transcription regulation; DNA-binding; Nuclear protein; Zinc-finger; Multigene family; Alternative splicing.
                    Nagpal S., Zelent A., Chambon P., "RAR-beta 4, a retinoic acid receptor isoform is generated from RAR-beta 2 by alternative splicing and usage of a CUG initiator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LKACLSGFTQAEWQHRHTAQS (IN ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 482;
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MISSING (IN ISOFORM BETA-4).
LNA -> MEN (IN ISOFORM BETA-4).
S -> T (IN ISOFORM BETA-1).
MISSING (IN ISOFORM BETA-1).
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Pred. No. 8.4e-122;
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PIR; $13515; $13516.
PIR; $13516; $13517.
PIR; $13517; $13517.
PIR; $05051; $05051.
HSSP; P10826; 1HRA.
PRANSERA; $700717; --
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Interpro; IPR000359; Hormone_rec_lig.
Interpro; IPR001723; Stdhrmn_receptor.
Interpro; IPR001628; Znf_C4sterold.
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MEDLINE-92212900; PubMed-1313565;
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PRINTS; PR00047; STROIDFINGER.
ProDom; PD000035; Znf_C4steroi
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Pfam; PF00105; zf-C4; 1.
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76.1%;
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SMART; SM00399; ZnF_C
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482 AA;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Coturnix coturnix japonica (Japanese quail).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            433
                                                                                                                                   106 LPPPRVYKPCFVCQDKSSGYHYGVSACEGCKGFFRRSIQKNMIYTCHRDKNCVINKVTRN 165
                                                                                                                                                                                                                                                                                                                                                         TLLKAACLDILILRICTRYTPEQDTMTFSDGLTLNRTQMHNAGFGPLTDLVFAFANQLLP 313
                                                                                                                                                                                                                                                                                                                                                                                                                                     LEMDDAETGLLSAICLICGDRQDLEQPDRVDMLQEPLLEALKVYVRKRRPSRPHMFPKML 373
                                                                        GHPPPSGCSTPSPASVGQACQRTTGGSQFAASTKWTPSLNAAIETQSTSSEELVPSPPSP 105
                                                                                                                 PPLPRIYKPCFVCQDKSSGYHYGVSACEGCKGFFRRSIQKNMVYTCHRDKNCIINKVTRN 133
                                                                                                                                                                                               PCQYCRLQKCFEVGMSKESVRNDRNKKKKEVPKPECSESYTLTPEVGELIEKVRKAHQET 193
                                       Fu Z.W., Kato H., Sugahara K., Kubo T.; "Molecular cloning of two isoforms of Japanese quail RAR beta and their expression profile during embryogenesis and in the developing
                                                                                                                                                                                                                     166 RCQYCRLQKCFEVGMSKESVRNDRNKKKKEPSKQECTESYEMTAELDDLTEKIRKAHQET
                                                                                                                                                                                                                                                                                                FPALCQLGKYTTNNSSEQRVSLDIDLWDKFSELSTKCIIKTVEFAKQLPGFTTLTIADQI
                                                                                                                                                                                                                                                                                                                                                                              MKITDLRSISAKGAERVITLKMEIPGSMPPLIQEMLENSEGLDTLSGQPGGGGRDGGGLP
29;
Indels
46;
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15-JUN-2002 (Rel. 41, Last annotation update)
Retinoic acid receptor beta (RAR-beta).
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Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                434 PPPGSCSPSLSPSSNRSSPATHSP 457
31;
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15-JUN-2002 (Rel. 41, Last seq
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBFAMILY.
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Matches 338;
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Q9W6B3;
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11D RRB_C

12 JUD RRB_C

15 JUD DT 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               390 VITLKMEIPGSMPPLIQEMLENSEGLDTLSGQPGGGGRDGGGLPPPPGSCSPSLSPSSNR 449
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Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              150 KESVRNDRNKKKKEVPKPECSESYTLTPEVGELIEKVRKAHQETFPALCQLGKYTTNNSS 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRYTPEQDIMIFSDGLILNRIQMHNAGFGPLIDLVFAFANQLLPLEMDDAETGLLSAICL 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Receptor; Transcription requiation; DNA-binding; Nuclear protein; Zinc-finger; Multigene family; Alternative splicing.
DNAIN 1 87 MODILATING (BY SIMILARITY).
DNA_BIND 88 153 MODILEAR RECEPTOR-TYPE.
ZN_FING 124 148 C4-TYPE.
ZN_FING 124 148 C4-TYPE.
DOMAIN 154 199 HINGE (BY SIMILARITY).
DOMAIN 200 419 LIGAND-BINDING (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PEKGLPAPGPYSTPLRTPLWNGSNHSIETQSSSSEEIVPSPPSPPPLPRIYKPCFVCQDK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HINGE (BY SIMILARITY).
LIGAND-BINDING (BY SIMILARITY).
608951B106C4CD41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71.2%; Score 1736; DB 1; 77.3%; Pred. No. 1.5e-120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RRB_CHICK STANDARD; PRT; 455 AA. P22448; Q90598; P27537; Q91354; 01-340-1991 (Rel. 19, Created) 15-741-1998 (Rel. 36, Last sequence update) 36-MAY-2000 (Rel. 39, Last annotation update) Retinoic acid receptor beta (RAR-beta).
    (See
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32; Mismatches
  entities requires a license agreement (or send an email to license@lsb-sib.ch)
                                                                                                                                                                                                                                                                                                              PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
                                                                                                          Interpro; IPR000536; Hormone_rec_lig.
Interpro; IPR001628; Znf_C4steroid.
Pfam; PF00104; hormone_rec; 1.
Pfam; PF00105; zf-C4; 1.
                                                                                                                                                                                                                PRINTS; PRO0047; STROIDFINGER.
ProDom; PD000035; Znf_C4steroid; 1.
                                                                     EMBL; AF110729; AAD23397.1; -.
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SMART; SM00399; ZnF_C4;
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EMBL; X59473; CAA42077.1; EMBL; S63196; AAB19628.1;

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SUBCELLUIAR LOCATION: NUCLEAR AND SELA-1 (SHOWN HERE) AND BETA-2;
ARE PRODUCTS: 2 ISOFORMS; BETA-1 (SHOWN HERE) AND BETA-2;
DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
A DAA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
NR1 SUBPAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-91347912; PubMed-1652423;
MEDLINE-91347912; PubMed-1652423;
MEDLINE-91347912; PubMed-1652423;
Meve A., Richman J.M., Brickell P.M.;
Retinoic acid treatment alters the distribution of retinoic acid receptor-beta transcripts in the embryonic chick face.";
Development 111:1007-1016(1991).

-I FUNCTION: THIS 1S A RECEPTOR FOR RETINOIC ACID. THIS METABOLITE HAS PROFOUND EFFECTS ON VERTEBBATE DEVELOPMENT. RETINOIC ACID IS A MORPHOGEN AND IS A POWERFUL TERATOGEN. THIS RECEPTOR CONTROLS CELLS FUNCTIONS BY DIRECTLY REGULATING GENE EXPRESSION.
                                                                                        ., Solursh M.; chicken retinoic acid binding
                                                                                                                                                                                                                                                                                                                                                                                          Ø
                                                                                                                                                                                       MEDLINE-91274365; PubMed-1647216;
Nohno T., Muto K., Noj1 S., Saito T., Taniguchi S.;
"Isoforms of retinoic acid receptor beta expressed in the chicken
                                                                                                                                                                                                                                                                                                                                                                                        þe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Differential expression of retinoic acid receptor-beta isoforms during chick limb ontogeny.";
Dev. Dyn. 202:54-66(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-91199956; PubMed-1849811;
Smith S.M., Elchele G.;
"Temporal and regional differences in the expression pattern distinct retinoic acid receptor-beta transcripts in the chick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-59 FROM N.A. (ISOFORM BETA-1).
MEDLINE-95218230; PubMed-7703521;
Smith S.M., Kirstein I.J., Wang Z.S., Fallon J.F., Kelley J.,
Bradshaw-Rouse J.,
                                                                                                                                                                                                                                                                                                          STRAIN-White leghorn,
MEDLINE-91163640; PubMed=1848357;
Noji S., Nohno T., Koyama E., Muto K., Ohyama K., Aoki Y.,
Tamura K., Ohsugi K., Ide H., Taniguchi S., Saito T.,
"Retinoic acid induces polarizing activity but is unlikely
morphogen in the chick limb bud.";
                                                                                                                                                                       SEQUENCE FROM N.A. (RAR-BETA-1 AND RAR-BETA-2).
                                                                                                                                                                                                                                                          Biochim. Biophys. Acta 1089:273-275(1991)
                                                                                   Padanilam B.J., McLeod L.B., Suzuki H.,
Nucleotide sequence of an isoform of ch
Protein-beta varying in its A domain.",
Nucleic Acids Res. 19:395-395(1991)
                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM BETA-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM BETA-2)
                                                                       MEDLINE-91195065; PubMed-1849630;
                                                   SEQUENCE FROM N.A. (RAR-BETA-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Development 111:245-252(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 350:83-86(1991).
                   CBI_TaxID=9031;
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EMBL; X57341; CAA40617.1; -. EMBL; X57340; CAA40616.1; -. EMBL; X57339; CAA40615.1; -. EMBL; S75943; AAB33959.1; -. EMBL; X56674; CAA39997.1; -.

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LIGAND-BINDING (BY SIMILARITY).
MITSSRTCPVPAVNGHMTHYPAAPYPLLFPPVIGGLSLPSL
HGLQSHPPTSGCSTPSPAT -> MFDCMDVLAVSPAQMLDF
YTASFSSCMLQEKALKACFSGLAQTEWQHRHSAQS (IN
                                                                                                                                                                                                                                                                                                                                                                                                                 150 KESVRNDRNKKKKEVPKPECSESYTLTPEVGELIEKVRKAHQETFPALCQLGKYTTNNSS 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     330 ICGDRQDLEQPDRVDMLQEPLLEALKVYVRKRRPSRPHMFPKMLMKITDLRSISAKGAER 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             444
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                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                        49 PTSGCSTPSP------ATVETQSTSSEELVPSPEPPPPRVXKPCFVCQDK 94
                                                                                                             30 PEKGLPAPGPYSTPLRTPLWNGSNHSIETQSSSSEEIVPSPPSPPPLPRIYKPCFVCQDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   210 EQRVSLDIDLWDKFSELSTKCIIKTVEFAKQLPGFTTLTIADQITLLKAACLDILLLRIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        270 TRYTPEQDIMIFSDGLTLNRTQMHNAGFGPLTDLVFAFANQLLPLEMDDAETGLLSAICL
                                                                                                                                                                                                                                                                                                                                      Length 455;
                                                                                                                                                                                                                                                                                                                                                          41; Indels
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S -> T (IN REF. 4).
E -> D (IN REF. 6).
819F6083ECA50610 CRC64;
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                                                                                                                                                                                                                                                                                                                                     71.1%; Score 1733; DB 1; 77.1%; Pred. No. 2.5e-120;
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                                                                                                                                                                                                                                                                                                                                                         33; Mismatches
     EMBL, S63136; AAB19628.1; -...
PIR; S13512; S13512.
PIR; S14291; S14291.
HSSP, P108026; IHRA.
InterPro; IPR001536; Hormone_rec_lig.
InterPro; IPR001723; Stdhrmn_receptor.
InterPro; IPR001783; Stdhrmn_receptor.
                                                                                              PRINTS, PRO0398; STRDHORMONER.
PRINTS; PRO0047; STROIDFINGER.
ProDom; PD000035; Znf_C4steroid; 1.
                                                                           Pfam; PF00104; hormone_rec; 1.
Pfam; PF00105; zf-C4; 1.
                                                                                                                                                                                                                                                                                                                  50708 MW;
                                                                                                                                                                                                                                                                                                                                                        Conservative
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108
148
199
419
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103
173
455 AA;
                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                        Matches 330;
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CONFLICT
SEQUENCE
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VARSPLIC
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DOMAIN
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Conformational adaptation of agonists to the human nuclear receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-91042616; PubMed-2172793;
MEDLINE-91042616; PubMed-2172793;
Ishikawa T., Umesono K., Mangelsdorf D.J., Aburatani H., Stanger E
Shibasaki Y., Imawari M., Evans R.M., Takaku F.;
"A functional retinoic acid receptor encoded by the gene on human
                                                                                                                                 PAKQLPGFTTLTIADQITLLKAACLDILLILRICTRYTPEQDTMTFSDGLTLNRTQMHNAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostom1; Catarrhin1; Hominidae; Homo.
                                                       PEVGELJEKVRKAHQETFPALCQLGKYTTNNSSEQRVSLDIDLWDKFSELSTKCIIKTVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Crystal structure of the RAR-gamma ligand-binding domain bound all-trans retinoic acid.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            acid receptor gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-89315787; PubMed-2546152;
Krust A., Kastner P., Petkovich M., Zelent A., Chambon
Krust A., Kastner P., Petkovich M., Zelent A., Chambon
"A third human retinoic acid receptor, hRAR-gamma.";
Proc. Natl. Acad. Sci. U.S.A. 86:5310-5314(1989).
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                                                                                                                                                                                                                                                                                                                                                     417 TLSGQPGGGGRDGGGLPPPPGSCSPSLSPSSNRSSPATHS 456
                                                                                                                                                                                                                                                                                                                                                                                         412 DQSEATEKKPEPEPPPPPPALLTMKKEQEDEDDSWATEN 451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        U1-JAN-1990 (Rel. 13, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Retinolc acid receptor gamma-1 (RAR-gamma-1).
RANG OR NR1B3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RAR gamma.";
Nat. Struct. Biol. 5:199-202(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-98162555; PubMed-9501913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mol. Endocrinol. 4:837-844(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RRG1_HUMAN STANDARD; I
P13631;
01-JAN-1990 (Rel. 13, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 378:681-689(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chromosome 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
RRG1_HUMAN
                                113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- SUBCELLULAR LOCATION: Nuclear.
-i- DOMAIN: COMPOSED OF THREE DOWAINS: A MODULATING N-TERMINAL DOMAIN,
A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
-i- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
NR1 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119 CHRDKNCIINKVTRNPCQYCRLQKCFEVGMSKESVRNDRNKKKKEVPKPEC--SESYTLT 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13; Gaps
                                                                                                                                                                                                                                                                                                                            receptors during zebrafish embryogenesis.";
Mech. Dev. 46:137-150(1994)
-i- FUNCTION: THIS IS A RECEPTOR FOR RETINOIC ACID. THIS METABOLITE
HAS PROFOUND EFFECTS ON VERTEBRATE DEVELOPMENT. RETINOIC ACID IS
A MORPHOGEN AND IS A POWERFUL TERATOGEN. THIS RECEPTOR CONTROLS
CELLS FUNCTIONS BY DIRECTLY REGULATING GENE EXPRESSION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MYESVEVGGPTPNPFLVVDFYNQNRACLLPEKGLPAPGPYSTPLRTPLWNG--SNHSIET 58
                                                                                                                   Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00031; NUCLEAR RECEPTOR; 1. Receptor; Transcription regulation; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 1663.5; DB 1; Length 499;
; Pred. No. 3.7e-115;
37; Mismatches 82; Indels 13;
                                                                                                                                                                                                                                                  MEDLINE-95001557; PubMed-7918098;
Joore J., der Lans G.B., Lanser P.H., Vervaart J.M., Zivkovic
Speksnijder J.E., Kruijer W.;
"Effects of retinoic acid on the expression of retinoic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HINGE.
LIGAND-BINDING.
83540619FB45A537 CRC64;
                                                                                            Retinoic acid receptor gamma (RAR-gamma) (ZRAR gamma).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEAR RECEPTOR-TYPE
C4-TYPE.
C4-TYPE.
                                         15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MODULATING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            188 HJ
409 LJ
56178 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; S74156; AAB32277.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZnF_C4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 328; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76
142
97
137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00430; HOLI;
SMART; SM00399; ZnF_C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            143~ 1
189 4
499 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HEA.
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                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSFAC; T04895;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA_BIND
ZN_FING
ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                   modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4,
            HAS PROPOUND EFFECTS ON VERTEBRATE DEVELOPMENT. RETINOIC ACID IS A MORPHOGEN AND IS A POWBERUL TERATOGEN. THIS RECEPTOR CONTROLS A MORPHOGEN AND IS A POWBERUL TERATOGEN. THIS RECEPTOR CONTROLS SUBCELLULAR LOCATION: NUCLEAR.

ALTERNATIVE RODUCTS: 2 isoforms; RAR-gammal (shown here) and RAR-gammal (AC P22932); are produced by alternative splicing. They DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN, A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN. NRI SUBFAMILY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPPSPPPLPRIYKPCFVCQDKSSGYHYGVSACEGCKGFFRRSIQKNMVYTCHRDKNCIIN 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KVTRNPCQYCRLQKCFEVGMSKESVRNDRNKKKKEVPKPECSESYTLTPEVGELIEKVRK 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AHQETFPALCQLGKYTTNNSSEQRVSLDIDLWDKFSELSTKCIIKTVEFAKQLPGFTTLT 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: THIS IS A RECEPTOR FOR RETINOIC ACID. THIS METABOLITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PEKGLPAPG-PYSTP-----LRTPLWNG-----SNHSIETQSSSSEEIVP 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00011, NUCLEAR RECEPTOR; 1.
Receptor; Transcription regulation; DNA-binding; Nuclear protein; Zinc-finger; Multigene family; Alternative splicing; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1EE27B22772D4AFD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MODULATING.
NUCLEAR RECEPTOR-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1662; DB 1;
Pred. No. 4.2e-115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68.2%; Scor.
72.8%; Pred. No. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001536; Hormone_rec_lig.
InterPro; IPR001723; Stdhrmn_receptor.
InterPro; IPR0010529; Znf_C45teroid.
Ffam; PF00104; hormone_rec; 1.
Pfam; PF00104; part 1.
Pfint; PR001398; STRDHORMONER.
PRINTS; PR00047; STROIDFINGER.
ProDom; PD000035; Znf_C45teroid; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C4-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C4-TYPE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50341 MW;
                                                                                                                                                                                                                                                                                                              EMBL; M24857; AAA52692.1; --
EMBL; M38258; AAA60254.1; --
EMBL; M57707; AAA63254.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 319; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00430; HOLI; 1.
SMART; SM00399; ZnF_C4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genew; HGNC:9866; RARG.
MIM; 180190; -.
                                                                                                                                                                                                                                                                                                                                                                          PIR; A35573; A35573.
PIR; S26848; S26848.
PDB; 3LBD; 02-MAR-99.
PDB; 4LBD; 02-MAR-99.
                                                                                                                                                                                                                                                                                                                                                            PIR; A33903; A33903.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126
156
202
454 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSFAC; T00720;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSFAC; T01330;
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ZN_FING
ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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375
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                                                                                                                                                             SUBCELLULAR LOCATION: NUCLEAR.
ALTERNATIVE PRODUCTS: 2 isoforms; RAR-gammal (AC P13631) and RAR-gammal (shown here); are produced by alternative splicing. They differ only in their N-terminal regions.
DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN, A DAN-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
NR1 SUBPAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Conformational adaptation of agonists to the human nuclear receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAT. STLUCT. BIO1. 5:199-202(1998).

-I. FUNCTION: THIS IS A RECEPTOR FOR RETINOIC ACID. THIS METABOLITE
HAS PROFOUND EFFECTS ON VERTEBRATE DEVELOPMENT. RETINOIC ACID IS
A MORPHOGEN AND IS A POWERFUL TERATOGEN. THIS RECEPTOR CONTROLS
CELLS FUNCTIONS BY DIRECTLY REGULATING GENE EXPRESSION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Renaud J.-P., Rochel N., Ruff M., Vivat V., Chambon P., Gronemeyer
                316 GQLLPLEMDDTETGLLSAICLICGDRMDLEEPERVDKLQEPLLEALRLYARRRPSQPYM
 IADQITLLKAACLDILILRICTRYTPEQDTMTFSDGLTLNRTQMHNAGFGPLTDLVFAFA
                                                                     309 NQLLPLEMDDAETGLLSAICLICGDRQDLEQPDRVDMLQEPLLEALKVYVRKRRPSRPHM
                                                                                                                                          369 FPKMLMKITDLRSISAKGAERVITLKMEIPGSMPPLIQEMLENSEGLDTLSGQPG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Crystal structure of the RAR-gamma ligand-binding domain bound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-63 FROM N.A.
MEDLINE=90207264; PubMed=2157210;
Kastner P., Krust A., Mendelsohn C., Garnier J.M., Zelent A.,
Leroy P., Staub A., Chambon P.;
"Mutine isoforms of tetinoic acid receptor gamma with specific patterns of expression.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chambon P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zelent A., Chambon P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 51-443 FROM N.A.
MEDINE-89315787; PubMed-2546152;
KTUST A., Kastner P., Petkovich M., Zelent A., Chambo
"A third human retinoic acid receptor, hRAR-gamma.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-98162555; PubMed-9501913;
Klaholz B.P., Renaud J.-P., Mitschler A., Zusi C.,
Gronemeyer H., Moras D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 167-412.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 87:2700-2704(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 167-412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 86:5310-5314(1989)
                                                                                                                                                                                                                                                                                                                                                                                                              15-JUN-2002 (Rel. 41, Last annotation update) Retinoic acid receptor gamma-2 (RAR-gamma-2).
                                                                                                                                                                                                                                                                                                                                            443 AA.
                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                               -----GGGRDGGGLPPP 435
                                                                                                                                                                                                                                                   436 SSEDEVPGGQGKGGLKSP 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       all-trans retinoic acid.";
                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 378:681-689(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   RARG OR NR1B3
                                                                                                                                                                                                                                                                                                                                         RRG2_HUMAN
P22932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RAR gamma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Moras D.;
                                                                                                                                                                                                                                                                                                                            RRG2_HUMAN
249
                                                                                                                                                                                                                 424
                                                                                                                                                                                                                                                                                                       RESULT 13
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RRG1_MOUSE
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or send an email to licenseélsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VYTCHRDKNCIINKVTRNPCQYCRLQKCFEVGMSKESVRNDRNKKKKEVPKPECSESYTL 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TPEVGELIEKVRKAHQETFPALCQLGKYTTNNSSEQRVSLDIDLWDKFSELSTKCIIKTV 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EFAKQLPGFTTLTIADQITLLKAACLDILLRICTRYTPEQDTMTFSDGLTLNRTQMHNA 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GFGPLTDLVFAFANQLLPLEMDDAETGLLSAICLICGDRQDLEQPDRVDMLQEPLLEALK 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VYVRKRRPSRPHMFPKMLMKITDLRSISAKGAERVITLKMEIPGSMPPLIQEMLENSEGL 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51
                                                                                                                                                                                                                                                                                                                                                                                 Receptor; Transcription regulation; DNA-binding; Nuclear protein; Zinc-finger; Multigene family; Alternative splicing; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MYESVEVGGPTPNPFLVVDFYNQNRACLLPEKGL---PAPPGPYSTPLRTPLW--NGSNHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56 IETQSSSSEEIVPSPPSPPPLPRIYKPCFVCQDKSSGYHYGVSACEGCKGFFRRSIQKNM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MYDCMETFAPGPRRLY-----GAAGPGAGLLRRATGGSCFAGLESFAWPQPASLQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4D709194F5111E86 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                               MODULATING.
NUCLEAR RECEPTOR-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 1655.5; DB 1
; Pred. No. 1.2e-114;
35; Mismatches 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIGAND-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------GGGRDGGGLPPP 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000536; Hormone_rec_lig.
InterPro; IPR001723; Stdhrmn_receptor.
InterPro; IPR001628; Znf_C4steroid.
Pfam; PF00104; hormone_rec; 1.
Pfam; PF00105; zf-C4; 1.
                                                                                                                                                                                                                                                                                                                          ProDom; PD000035; Znf_C4steroid; 1.
SMART; SM00430; HOLI; 1.
SMART; SM00399; ZnF_C4; 1.
PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                          C4-TYPE.
C4-TYPE.
                                                                                                                                                                                                                                                                                          PRINTS, PR00398; STRDHORMONER.
PRINTS; PR00047; STROIDFINGER.
ProDom; PD000035; Znf_C4steroid; 1.
                                                                                                                           EMBL; M24857; -; NOT_ANNOTATED_CDS.
EMBL; M32074; AAA60253.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HINGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49307 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67.9%;
71.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 323; Conservative
                                                                                                                                                                                                Genew; HGNC:9866; RARG
MIM; 180190; -.
                                                                                                                                                                       02-MAR-99.
                                                                                                                                                         3LBD; 02-MAR-99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               443 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                      PDB; 4LBD; 02-MAR·
TRANSFAC; T00720;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DTLSGQPG---
                                                                                                                                                                                                                                                                                                                                                                                                                             DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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ZN_FING
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               This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: Nuclear.
-!- ALTERNATURE PRODUCTS: 2 ISOCORMS; RAR-GAMMA-A (SHOWN HERE) AND
RAR-GAMMA-B (AC P2078); ARE PRODUCED BY ALTERNATURE SPLICING.
-!- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
                                                                                                                                                                                                                 Zelent A., Krust A., Petkovich M., Kastner P., Chambon P.; "Cloning of murine alpha and beta retinoic acid receptors and a novel receptor gamma predominantly expressed in skin."; Nature 339:714-717(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN. SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-90220619; PubMed-2157970;
Giguere V., Shago M., Zirngibl R., Tate P., Rossant J., Varmuza £
"Identification of a novel isoform of the retinoic acid receptor gamma expressed in the mouse embryo.";
                              (Rel. 16, Created)
(Rel. 17, Last sequence update)
(Rel. 40, Last annotation update)
                                                                            Retinoic acid receptor gamma-A (RAR-gamma-A)
   458 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGD; MGI:97858; Rarg.
InterPro; IPR000356; Hormone_rec_lig.
InterPro; IPR00123; Stdhrmn_receptor.
InterPro; IPR001628; Znf_C4steroid.
                                                                                                                                                                                                                                                                                                                                                                            Cell. Biol. 10:2335-2340(1990)
                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-89295563; PubMed-2544807;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00398; STRDHORMONER PRINTS; PR00047; STROIDFINGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00104; hormone_rec; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X15848; CAA33845.1; -. EMBL; M34476; AAA40035.1; -.
                                                                                                                                                                                                                                                                                                                                                                                            [3]
SEQUENCE OF 1-74 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M32068; AAA40032.1;
                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P22932; 3LBD.
TRANSFAC; T00717; -.
TRANSFAC; T01340; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A34714; A34714
A35991; A35991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NR1 SUBFAMILY.
                                                                                                                                                      NCBI_TaxID=10090;
                                                                                           RARG OR NR1B3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF00105
                            01-NOV-1990
                                              01-FEB-1991
                                                           16-OCT-2001
RRG1_MOUSE
P18911;
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ZN_FING
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Matches
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       NOTE THE TENT OF T
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                                                                                                                                                                                                                                                                                                                                                                                                                     423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            249 IADQITLLKAACLDILILRICTRYTPEQDIMIFSDGLTLNRTQMHNAGFGPLTDLVFAFA 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   309 NOLLPLEMDDAETGLLSAICLICGDRODLEQPDRVDMLQEPLLEALKVYVRKRRPSRPHM 368
                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                    68
                                                                                                                                                                                                                                                                                                                                                                                   16 PGSGYPGAGFPFAFPGALRGSPPFEMLSPSFRGLGQPDLPKEMASLSVETQSTSSEEMVP 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   s.;
Probom; Fuccost, 1.
SWART; SMO0430; HOLI; 1.
SWART; SMO0399; ZnF_C4; 1.
PROSITE; PSO0031; NUCLEAR_RECEPTOR; 1.
Receptor; Transcription regulation; DNA-binding; Nuclear protein; Zinc-finger; Multigene family; Alternative splicing.

MODULATING.

MODULATING.

I 89 MODULATING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30 PEKGLPAPG-PYSTP-----LRTPLWNG-----SNHSIETQSSSSEEIVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              129 KVTRNPCQYCRLQKCFEVGMSKESVRNDRNKKKKEVPKPECSESYTLTPEVGELIEKVRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      189 AHQETFPALCQLGKYTTNNSSEQRVSLDIDLWDKFSELSTKCIIKTVEFAKQLPGFTTLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           369 FPKMLMKITDLRSISAKGAERVITLKMEIPGSMPPLIQEMLENSEGLDTLSGQPG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Mus
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-90220619; PubMed-2157970;
Giguere V., Shago M., Zirngibl R., Tate P., Rossant J., Varmuza & Giguere V., Shago M., Zirngibl R., Tate P., Rossant J., Varmuza & "Identification of a novel isoform of the retinoic acid receptor gamma expressed in the mouse embryo.";
Mol. Cell. Biol. 10:2335-2340(1990).
                                                                                                                                                                                                                                                                                                                32;
                                                                                                                                                                                                                                                                            Length 458;
                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                       DPAK -> RPSQ (IN REF. 1).
F4B63FCF80697636 CRC64;
                                                                                                                                                                                                                                                                        ; Score 1642; DB 1;
; Pred. No. 1.3e-113;
41; Mismatches 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Retinoic acid receptor gamma-B (RAR-gamma-B).
                                                                                                                                                                                                      LIGAND-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   447 AA.
                                                                                                                                                                 C4-TYPE.
                                                                                                                                                                                   HINGE
                                                                                                                                                                                                                                        50834 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      424 -----GGGRDGGGLPPPP 436
                                                                                                                                                                                                                                                                          67.4%;
71.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        436 SSEDEAPGGQGKRGQSPQP 454
                                                                                                                                                                                                                                                                                                              Matches 315; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                        155
110
150
201
421
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                                                                                                                                                                                                                                  458 AA;
                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                            90
126
156
202
369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RRG2_MOUSE
P20787;
                                                                                                                         DNA_BIND
ZN_FING
ZN_FING
DOMAIN
                                                                                                                                                                                                                   CONFLICT
                                                                                                                                                                                                                                                                        Match
                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                    DOMAIN
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                                                                                                                                                                                                                                                                                                                -!- SUBCELLULAR LOCATION: Nuclear.
-!- ALTERNATIVE PRODUCTS: 2 ISOPORMS; RAR-GAMMA-B (SHOWN HERE) AND
RAR-CAMMA-A (AC P18911); ARE PRODUCED BY ALTERNATIVE SPLICING.
-!- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
A DAR-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
-!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
NR1 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNHSIETQSSSSEEIVPSPPSPPPEPRIYKPCFVCQDKSSGYHYGVSACEGCKGFFRSI 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48 SLOSVETQSTSSEEMVPSSPSPPPPRVYKPCFVCNDKSSGYHYGVSSCEGCKGFFRRSI 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        232 IKTVEFAKQLPGFTTLFIADQITLLKAACLDILILRICTRYTPEQDTMTFSDGLTLNRTQ 291
                                                                                                                                          patterns of expression.";
Proc. Natl. Acad. Sci. U.S.A. 87:2700-2704(1990)
-!- FUNCTION: THIS IS A RECEPTOR FOR RETINOIC ACID. THIS METABOLITE
HAS PROFOUND EFFECTS ON VERTEBRATE DEVELOPMENT. RETINOIC ACID IS
A MORPHOGEN AND IS A POWERFUL FERATGCEN. THIS RECEPTOR CONTROLS
CELLS FUNCTIONS BY DIRECTLY REGULATING GENE EXPRESSION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SYTLTPEVGELIEKVRKAHQETFPALCQLGKYTTNNSSEQRVSLDIDLWDKFSELSTKCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              168 SYELSPQLEELITKVSKAHQETFPSLCQLGKYTTNSSADHRVQLDLGLWDKFSELATKCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11;
SEQUENCE OF 1-63 FROM N.A.
MEDLINE=90207264; PubMed=2157210;
Kastner P., Krust A., Mendelsohn C., Garnier J.M., Zelent A.,
Leroy P., Staub A., Chambon P.;
"Murine isoforms of retinoic acid receptor gamma with specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
Receptor; Transcription regulation; DNA-binding; Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9C45518BC38DAA99 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Multigene family; Alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEAR RECEPTOR-TYPE. C4-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 1633.5; DB 1;
; Pred. No. 5.2e-113;
34; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIGAND-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD; MGI:97858; Rarg.
InterPro; IPR000536; Hormone_rec_lig.
InterPro; IPR001723; Stdhrmn_receptor.
InterPro; IPR0010723; Stdhrmn_receptor.
Pfam; PF00104; hormone_rec; 1.
Pfam; PF00105; STG-C4; 1.
PRINTS; PR00398; STRDHORMONER.
PRINTS; PR00047; STROIDFINGER.
ProDom; PD000035; Znf_C4steroid; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MODULATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C4-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HINGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49792 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M34475; AAA40036.1; -. EMBL; M32069; AAA40033.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C4; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; B34714; B34714.
PIR; B35991; B35991.
HSSP; P22932; 3LBD.
TRANSFAC; T00717; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00430; HOLI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SM00399; ZnF_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79
115
145
191
447 AA;
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les 308; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRANSFAC; T01341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zinc-finger;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA_BIND
ZN_FING
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Db 228 IKIVEFAKRLPGFTGLSIADQITLLKAACLDILMLRICTRYTPEQDTMTFSDGLTLNRTQ 287

Qy 292 MHNAGFGPLTDLVFAFANQLPLEMDDAFTGLLSAICLICGDRQDLBQPDRVDMLQEPLL 351

Db 288 MHNAGFGPLTDLVFAFAGQLLPLEMDDAFTGLLSAICLICGDRWDLEEPEKVDMLQEPLL 351

Qy 352 EALKVYVRRRPSRPHMFPKMLMKITDLRSISAKGAERVITLKMEIPGSMPFLIQEMLEN 411

Db 348 EALKYVRRRPSRPHMFPKMLMKITDLRSISAKGAERVITLKMEIPGPMPPLIREMLEN 411

Db 348 EALKYVRRRPSPKMFMFMKMITDLRSISAKGAERVITLKMEIPGPMPPLIREMLEN 407

Qy 412 SEGLDTLSGQDG------GGGRGGGLPPPP 436

Db 408 PEMFEDDSSKPGPHPKASSEDEAPGGGGRRGQSPQP 443
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Search completed: March 29, 2003, 06:39:39 Job time: 24 secs

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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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- protein search, using sw model OM protein

Run on:

US-09-691-220-2 2437 1 MYESVEVGGPTPNPFLVVDF.....SCSPSLSPSSNRSSPATHSP Perfect score:

Seguence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

Total number of hits satisfying chosen parameters: 283224 seqs, 96134422 residues Searched:

283224

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 73:* Database

pirl:* pir2:* pir3:* pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

retinoic acid rece hormone re hormone re hormone acidacid acid acid acid retinoic acid retinoic acid acid acid acid acid retinoic acid Description retinoica retinoica retinoica retinoic a retinoic retinoic thyroid h probable retinoic retinoic retinoic retinoic chyroid chyroid thyroid hyroid SUMMARIES S78481 C40045 I50674 S02827 S05051 A43786 S13512 I51257 A333903 C35991 A38592 S06124 B41977 S02758 S09178 S14416 B36067 QRMSA1 A40917 VXLTA Length DB Match 2124.5 2119 2099 2089 2008.5 2008.5 2008.5 1972 1771 1757 1733 1663.5 1655.5 1655.5 1651.1631.1631.5 1627.5 1620.5 Score 724 658 657.5 653 653 652 652 Result Š.

thyroid hormone re thyroid hormone re	gene c-erba-beta p thyroid hormone re thyroid hormone re	thyroid hormone be thyroid hormone re	thyroid hormone re thyroid hormone re beta-thyroid hormo thyroid hormone re	thyroid hormone re transforming prote	transiorming prote thyroid hormone re
I51097 I51096 TVCHVR	151165 S06410 C36067	A57035 D36067 TVHIAR	TVCHTB S58211 A40377	A31820 TVFVVR	814418
777	000	226	1100	240	7 7
391 416 408	373 410 373	475 373 456	369 369 461	398	413
26.5	26.2 26.2 25.9	25.7 25.6 25.4	25.4 25.4 25.2	25.2	24.4
646.5 646 645.5	639 638 630	625.5 625 619.5	618 618 615	614.5	593.5
30 31 32	333 354 35	36 37 38	39 4 4 1 1 0 9	444	4 5

ALIGNMENTS

RESULT 1

A29491	retinoic acid receptor alpha - human	C;Species: Homo sapiens (man)	C;Date: 04-Jun-1999 #sequence_revision 04-Jun-1999 #text change 16-Jun-2000	C, Accession: A29491; S07272; S06224; S15598; A58975; A29740; S15599	R;Giguere, V.; Ong, E.S.; Sequi, P.; Evans, R.M.	Nature 330, 624-629, 1987	A; Title: Identification of a receptor for the morphogen retinoic acid.	A:Reference number: A29491: MITD.88065922: DMTD.2825036
			16-Jun-2000	599			acid.	

A; Molecule type: mRNA A; Residues: 1-462 <GIG>

A/Cross-references: GB:X06614; NID:g36156; PIDN:CAA29829.1; PID:g36157
R;Chambon, P.
Submitted to the EMBL Data Library, December 1988
A;Reference number: S07272
A;Reference number: S07272
A;Reference number: S07272
A;Rolecule type: mRNA
A;Rolecule type: mRNA
A;Residues: 31-462 <CHA>
A;CHA>
A;Cross-references: EMBL:X06538; NID:g35873; PIDN:CAA29787.1; PID:g35874
A;Cross-references: EMBL:X06538; NID:g35873; PIDN:CAA29787.1; PID:g35874
A;Petkovich, M.; Brand, N.J.; Krust, A.; Chambon, P.
A;Title: A human retinoic acid receptor which belongs to the family of nuclear recept
A;Reference number: S06224; MUID:88065872; PMID:2825025
A;Accession: S06224

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A; Molecule type: mRNA
A; Residues: 31-179, 'V., 181-462 <PET>
A; Residues: 31-179, 'V., 181-462 <PET>
A; Residues: 31-179, 'V., 181-462 <PET>
A; Residues: 231-179, 'V., 181-462 <PET>
A; Rote: this sequence has been revised in reference S07272
A; Note: the authors translated the codon AAC for residue 360 as Lys; the sequence sho A; Note: the authors translated the codon AAC for residue 360 as Lys; the sequence sho A; Note: the authors translated the codon, P.
A; Note: Cardia Res. 18, 6799-6806, 1990
A; Title: Characterization of a functional promoter for the human retinoic acid recept
A; Reference number: S15594; MUID:91088249; PMID:2175878

A; Accession: S15598

A;Molecule type: DNA Residues: 1-80 <BRAL> A;Crossreferences: EMBL:X56058; NID:g35876; PIDN:CAA39533.1; PID:g825712 A;Accession: A58975 A; Molecule type: DNA

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A;Cross-references: GB:X58685; NID:g35878; PIDN:CAA41532.1; PID:g1335286 A; Residues: 61-80 <BRA2>

A; Gene: GDB: RARA

rece

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hyroid

A; Cross-references: GDB:120337; OMIM:180240

A; Map position: 17q12-17q12

A;Note: the first intron occurs before the initiator codon; the list of introns is in C;Superfamily: retinoic acid receptor alpha; erzh transforming protein homology. C;Reywords: DNA binding; nucleus; transcription regulation; zinc finger F;86-337/Domain: erbA transforming protein homology // Fige-337/Domain: erbA transforming protein homology

28

239 238 299

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A; Residues: 1-955 CDET>
A; Cross-references: GB:S50916; NID:g234248; PIDN:AAB19602.1; PID:g234249
B; Cross-references: GB:S50916; NID:g234248; PIDN:AAB19602.1; PID:g234249
B; Rakizuka, A.; Miller Jr., W.H.; Umesono, K.; Warrell Jr., R.P.; Frankel, S.R.; Muri
Call 66, 663-674, 1991
A; Title: Chromosomal translocation t(15;17) in human acute promyelocytic leukemia fus
A; Reference number: A40044; MUID:91347368; PMID:1652368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable transcription factor PML/retinoic acid receptor alpha mutant fusion p C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: O5-Un-1992 #sequence_revision 17-Nov-1995 #text_change 20-Apr-2000
C; Accession: C40045; B40044
R; de The, H; Lavau, C; Marchio, A.; Chomienne, C.; Degos, L.; Dejean, A. Cell 66, 675-684, 1991
A;Title: The PML-RARalpha fusion mRNA generated by the t(15;17) translocation A; Reference number: A40045; MUID:91347369; PMID:1652369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: mRNA
A;Residues: 1-394,553-955 <KAK>
A;Residues: 1-394,553-955 <KAK>
C;Comment: This sequence is the chimeric product of a translocation mutation.
C;Genetics:
                                                                                                                                            RDKNCIINKVTRNPCQYCRLQKCFEVGMSKESVRNDRNKKKK;EVPKPECSESYTLTPEV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        360 KRRPSRPHMFPKMLMKITDLRSISAKGAERVITLKMEIPGSMPPLIQEMLENSEGLDTLS 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSSEEIVPSPPSPPFLPRIYKPCFVCQDKSSGYHYGVSACEGCKGFFRRSIQKNMVYTCH 120
                                                                                                                                                                                                                                                                                                                                                                                         LTDLVFAFANQLLPLEMDDAETGLLSAICLICGDRQDLEQPDRVDMLQEPLLEALKVYVR 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PEQPRPSTSKAVSPPHLDGPPSPRSPVIGSEVFLPNSNHVASGAGEAAIETQSSSSEEIV 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PSPPSPPPLPRIYKPCFVCQDKSSGYHYGVSACEGCKGFFRRSIQKNMVYTCHRDKNCII 127
                                                                                       180 GELIEKVRKAHQETFPALCQLGKYTTNNSSEQRVSLDIDLWDKFSELSTKCIIKTVEFAK
        240 OLPGFTTLTIADQITLLKAACLDILILRICTRYTPEQDTMTFSDGLTLNRTQMHNAGFGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87.0%; Score 2119; DB 4; 90.9%; Pred. No. 1.2e-147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30 PEKGLPA-----PGPYSTPLRTPLW-NGSNH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Map position: 15q22/17q12
C;Keywords: alternative splicing; fusion protein
F;57-227/Region: cysteine-rich
F;561-601/Region: zinc finger motif
F;617-641/Region: zinc finger motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: B40044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: PML/RARA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Sim
Matches 409;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                retinoic acid receptor alpha-2 - eastern newt
C;Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)
C;Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 20-Aug-1999
C;Accession: S78481; S26656
R;Ragsdale, C.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VPSPPSPPPLPRIYKPCFVCQDKSSGYHYGVSACEGCKGFFRRSIQKNMVYTCHRDKNCI 126
                                                                                                                                                                                                                                          72 VPSPPSPPPLPRIYKPCFVCQDKSSGYHYGVSACEGCKGFFRKSIQKNWYYTCHRDKNCI 131
                                                                                                                                                                                                                                                                                                        INKVTRNPCQYCRLQKCFEVGMSKESVRNDRNKKKKEVPKPECSESYTLTPEVGELIEKV 186
                                                                                                                                                                                                                                                                                                                           426
                                                                                                                                                                                                                                                                                                                                                                                     RKAHQETFPALCQLGKYTTNNSSEQRVSLDIDLWDKFSELSTKCIIKTVEFAKQLPGFTT 246
                                                                                                                                                                                                                                                                                                                                                                                                           FANQLLPLEMDDAETGLLSAICLICGDRODLEQPDRVDMLQEPLLEALKVYVRKRRPSRP 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R; Ragsdale Jr., C.W.; Gates, P.B.; Brockes, J.P.
Nucleic Acids Res. 20, 5851, 1992
A; Title: Identification and expression pattern of a second isoform of the A; Reference number: S26656, MUID: 93087213; PMID: 1333589
A; Accession: S2656
A; Status: nucleic acid sequence not shown
A; Molecule type: mRNA
A; Residues: 1-52 < RAW>
                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:214254
C;Superfamily: retinoic acid receptor alpha; erbA transforming protein |
C;Keywords: DNA binding; nucleus; transcription regulation; zinc finger
F;79-331/Domain: erbA transforming protein homology <ERBA>
F;81-101/Region: zinc finger CCCC motif
                                                                                                                                        VGGPTPNPFLVVDFYNQNRACLLPEKGLPAPGPYSTPLRTPLWNGSNHSIETQSSSSEEI
                                                                                                                                                                     HMFPKMLMKITDLRSISAKGAERVITLKMEIPGSMPPLIQEMLENSEGLDTLSGQPGGGG
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                                                              Length 462;
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; Pred. No. 1.8e-148;
29; Mismatches 23;
                                                          Score 2127; DB 1;
Pred. No. 1.2e-148;
5; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data Library, August 1992
A;Reference number: S78481
A;Accession: S78481
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87.1%;
                                                          Ouery Match 87.3%;
Best Local Similarity 91.6%;
Matches 413; Conservative
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Best Local Similarity ...
...hea 399; Conservative
F:88-108/Region: zinc finger F;124-148/Region: zinc finger
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A; Residues: 1-452 <RAG>
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Length 955; Indels ---SIETQSSSSEEIV 67

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A; Residues: 1-390, A; <KRU>
A; Cross-references: EMBL:X57528; NID:q53890; PIDN:CAA40749.1; PID:g53891
A; Cross-references: EMBL:X57528; NID:g53890; PIDN:CAA40749.1; PID:g53891
A; Experimental source: embryonic carcinoma cell line RAC65
A; Note: this is the entire sequence of a truncated rethnoic acid receptor alpha proc
R; Leroy, P.; Krust, A.; Zelent, A.; Mendelsohn, C.; Garnier, J.M.; Kastner, P.; Dier
EMBO J. 10, 59-69, 1991
A; Title: Multiple isoforms of the mouse retinoic acid receptor alpha are generated b; Reference number: S13599; MUID:91114713; PMID:1846598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cell line RAC65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C.E.; Feijen, A.; Jor
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A) Cross-references: GB:S56656; NID:g298621; PIDN:AAB25783.1; PID:g298622
C) Superfamily: retinoic acid receptor alpha; erbA transforming protein homology
C) Keywords: alternative splicing; DNA binding; nucleus; transcription regulation;
F; 86-337/Domain: erbA transforming protein homology <ERBA>
F; 88-108/Region: zinc finger
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   LTDLVFAFANOLLPLEMDDAETGLLSAICLICGDRODLEQPDKVDKLQEPLLEALKIYVR
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                                                                                                                                                                                                                                                                                                                                                               receptors
                                                                                                                                                                                                                                          retinoic acid nuclear receptor isoform alpha 1 - mouse c;Species: Mus musculus (house mouse) c;Date: O'Jun-1990 #sequence_revision 07-Jun-1990 #text_change c;Accession: 805050; 823797; 813599; 156594 R;Zelent, A.; Krust, A.; Petkovich, M.; Kastner, P.; Chambon, P. Mature 339, 714-717, 1989 A;Title: Cloning of murine alpha and beta retinoic acid receptors A;Reference number: 805050; MUID:89295563; PMID:2544807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L.J.; Mader, S.; van den Brink,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: mRNA
A;Residues: 1-73 <LER>
A;Cross-references: EMBL:X56572; NID:g53892; PIDN:CAA39919.1;
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Differentiation 49, 27-37, 1992
A;Title: Retinot co.d. resistance of the variant embryonal
A;Reference number: S23797; MUID:92324516; PMID:1320576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R; Heiermann, R.; Rentrop, M.; Lang, E.; Maelicke, A.
J. Recept. Res. 13, 693-709, 1993
A;Title: Cloning of several genes coding for retinoic acid
A;Reference number: 156594; MUID:93195858; PMID:8383767
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Pred. No. 7.7e-146;
8; Mismatches 17;
                                                                                                                 GQPGGGGRDGGGLPPPPGSCSPSLSPSSNRSSPATHSP 457
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                                                                                                                                    GQPGGPRT--GGLGPPPGSCSPSLSPSSTRSSPATHSP
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A,Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-462 <ZEL>
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90.0%;
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F)88-108/Region: zinc finger
F)124-148/Region: zinc finger
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               retinoic acid receptor alpha isoform 2-1 - chicken
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Bate: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 20-Aug-1999
C;Accession: 15067,
R;Michaille, JJ.; Kanzler, B.; Blanchet, S.; Garnier, J.M.; Dhouailly, D.
Int. J. Dev. Biol. 39, 587-596, 1995
A;Title: Characterization of cDNAs encoding two chick retinoic acid recepton
                                       187
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PSPPSPPPLPRIYKPCFVCQDKSSGYHYGVSACEGCKGFFRRSIQKNMVYTCHRDKNCII 625
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                                                        TIADQITLLKAACLDILILRICTRYTPEQDTMTFSDGLTLNRTQMHNAGFGPLTDLVFAF
                                                                                                                                                                                                         NKVTRNPCQYCRLQKCFEVGMSKESVRNDRNKKKKEVPKPECSESYTLTPEVGELIEKVR
                                                                                                             KAHQETFPALCQLGKYTTNNSSEQRVSLDIDLWDKFSELSTKCIIKTVEFAKQLPGFTTL
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A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-453 <MIC>
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88.0%;
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A; Molecule type: mRNA
A; Residues: 1-448 <SHA>
A; Cross-references: GB:X87365; GB:S53907; GB:S53908; NID:g836654; PIDN:CAA60791.1;
                                                                                                                                                                                                          A; Reference number: A56558; MUD:93144180; PMID:1336976
                                                                                                                                                                                                                                                                                                                                                                     A;Note: sequence extracted from .NCBI backbone (NCBIN:123871, NCBIP:123874) (S. Superfamily: retinoic acid receptor alpha; erbA transforming protein homology C;Reywords: zinc finger F;75-326/Domain: erbA transforming protein homology <ERBA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 retinote acid receptor alpha - zebra fish
C;Species: Brachydanio rerio (zebra fish)
C;Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 20-Aug-1999
C;Accession: I51256
R;Joore, J.; van der Lans, G.B.; Lanser, P.H.; Vervaart, J.M.; Zivkovic, D.; Sp.
Mech. Dev. 46, 137-150, 1994
A;Title: Effects of retinoic acid on the expression of retinoic acid receptors
                                                                                                                        retinoic acid receptor isoform alpha 2.2 - African clawed frog C;Species: Xenopus laevis (African clawed frog)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 20-Aug-1999
C;Accession: B56558
R;Sharpe, C.R.
Mech. Dev. 39, 81-93, 1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361 RRPSRPHMFPKMLMKITDLRSISAKGAERVITLKMEIPGSMPPLIQEMLENSEGLDTLSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 2026.5; DB 2, Pred. No. 2.9e-141;
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                       G---GGASSDAPVTPVAPGSCSPSLSPSSTHSSPSTHSP
     SGQPGGGGRDGGGLPPPGSCSPSLSPSSNRSSPATHSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                83.2%; Scor.
84.3%; Pred. No. 2...
22; Mismatches
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Matches 388; Conservative
                                                                                                                                                                                                                                                                                   A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A:Status: preliminary
A:Molecule type: mRNA
A:Molecule type: mRNA
A:Molecules: 1-464 < CSHA>
A:Experimental source: embryos
A:Note: sequence extracted from NCBI backbone (NCBIN:123865, NCBIP:123867)
C:Superfamily: retinoic acid receptor alpha; erba transforming protein homology
C:Keywords: Zinc finger
F:91-342/Domain: erbA transforming protein homology <
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 CHRDKNCIINKVTRNPCQYCRLQKCFEVGMSKESVRNDRNKKKKEVPKPECSESYTLTPE 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     179 VGELIEKVRKAHQETFPALCQLGKYTTNNSSEQRVSLDIDLMDKFSELSTKCIIKTVEFA 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             248
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                                                                                   307 FANQLLPLEMDDAETGLLSAICLICGDRQDLEQPDRVDMLQEPLLEALKVYVRKRRPSRP
                                                                                                                                                         HMFPKMLMKITDLRSISAKGAERVITLKMEIPGSMPPLIQEMLENSEGLDTLSGQPGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84.5%; Score 2058.5; DB 2; Length
85.6%; Pred. No. 1.4e-143;
ive 21; Mismatches 40; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      retinoic acid receptor alpha - African clawed frog C; Species: Xenopus laevis (African clawed frog) C; Species: Xenopus laevis (African clawed frog) C; Species: Amer-1993 #sequence_revision 18-Nov-1994 #text_change 07-Feb-1997 C; Accession: A4197; Mangelsdorf, D.J.; Dyck, J.A.; Bittner, D.A.; Evans, R.M.; I Proc. Natl. Acad. Sci. U.S.A. 89, 2321-2325, 1992 A.Title: Multiple retinoid responsive receptors in a single cell: families CA; Reference number: A41977; MUD:92196110; PMID:1312717 A; Recession: A41977
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                                                                                                                                                                                                                                                                                                                                                                                                    194 RVITLKMEIPGSMPPLIQEMLENSEGLDSLTGQP----PRASSLAPPPGSCSPSLSPSSN 449
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                                                                                                                                                                            KESVRNDRNKKKK-EVPKPECSESYTLTPEVGELIEKVRKAHQETFPALCQLGKYTTNNS
                                                                                                                             ----SPATIETQSTSSEEIVPSPPSPPPLPRIYKPCFVCQDK
                                               SSGYHYGVSACEGCKGFFRRSIQKNMVYTCHRDKNCIINKVTRNPCQYCRLOKCFEVGMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A.Molecule type: mRNA
A.Residues: 1-459 <BLUD
A.BOLE Seduces: 1-459 <BLUD
A.Note: Sequence extracted from NCBI backbone (NCBIP:88334)
A.Note: Sequence extracted from alpha; erbA transforming [C.Keywords: zinc finger
F:86-337/Domain: erbA transforming protein homology <ERBA>
F:88-108/Region: zinc finger
F:124-148/Region: zinc finger
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79.1%; Score 1926.5; DB 2
81.6%; Pred. No. 6.7e-134;
ive 17; Mismatches 43;
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Similarity
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450 RSSPTSHSP 458
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C;Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)
C;Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)
C;Accession: S06123
R;Ragsdale Jr., C.W.; Petkovich, M.; Gates, P.B.; Chambon, P.; Brockes, J.P.
Nature 341, 654-657, 1989
A;Title: Identification of a novel retinoic acid receptor in regenerative tissues of A;Reference number: S06123
A;Molecule type: mRNA
A;Residues: 1-458 <RAGS
A;Cross-references: EMBL:X17585; NID:g64125; PIDN:CAA35602.1; PID:g64126
C;Superfamily: retinoic acid receptor alpha; erbA transforming protein homology
C;Keywords: DNA binding; nucleus; transcription regulation; zinc finger
F;87-107/Region: zinc finger
F;123-147/Region: zinc finger
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                                                                                                                                    protein homology
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                                                                                                                                                                                                                                                                                                                                                          112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1913 TDLVFAFANQLLPLEMDDAETGLLSAICLLCGDRQDLEQADKVDVLQEPLLEALKIYVRN 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    412
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                                                                                                                                                                                                                         Gaps
                                                                                   A,Cross-references: GB:S74155; NID:9704369; PIDN:AAB32276.1; PID:9704370
C;Genetics:
                                                                                                                                                                                                                                                                              1 MYESVDV-----NPFLAMDYYNQSRGCLIPDK----MPHPFSSSIRHQHWSGSNHSIETQS
                                                                                                                                                                                                                                                                                                                                            ELIEKVRKAHQETFPALCQLGKYTTNNSSEQRVSLDIDLWDKFSELSTKCIIKTVEFAKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   233 LPGFTTLTIADQITLLKAACLDILILRICTRYTPEQDIMTFSDGLTLNRTQMHNAGFGPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RRPSRPHMFPKMLMKITDLRSISAKGAERVITLKMEIPGSMPPLIQEMLENSEGLDTLSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MYESVEVGGPTPNPFLVVDFYNQNRACLLPEKGLPAPGPYSTPLRTPLWNGSNHSIETQS
                                                                                                                                                                                                                        13;
                                                                                                                                                                                      82.4%; Score 2008.5; DB 2; Length 444; 82.9%; Pred. No. 6e-140; ive 35; Mismatches 30; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80.9%; Score 1972; DB 2; Length 458;
88.3%; Pred. No. 3e-137;
ive 16; Mismatches 18; Indels 1
                                                                                                                                      C;Superfamily: retinoic acid receptor alpha; erbA transforming F;73-324/Domain: erbA transforming protein homology <ERBA>
   A; Reference number: I51256; MUID:95001557; PMID:7918098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AQGSRAS----ATTPGSCSPSLSPNSAQSSPPTQSP 444
                 A;Accession: 151256
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-444 <JOO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       421 QPGGGGRDGGGLPPPPGSCSPSLSPSSNRSSPATHSP 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ilarity 88.3%;
Conservative
                                                                                                                                                                                                                         379; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 379; Conserv
                                                                                                                                                                                                          Similarity
                                                                                                                         A; Gene: zRARalpha
                                                                                                                                                                                        Query Match
Best Local S
Matches 379
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181

33 GLPAPGP----YSTPLRTPLWNGSNHSIETQSSSSEEIVPSPPSPPPLPRIYKPCFVCQDK 89

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C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Dates 107-Jun 1990 #sequence_revision 07-Jun-1990 #text_change 20-Aug-1999
C; Accession: 505051; S13516; S3040
R; Zelent, A.; Krust, A.; Petkovich, M.; Kastner, P.; Chambon, P.
Nature 339, 714-717, 1989
A; Title: Cloning of murine alpha and beta retinoic acid receptors and a novel recept. A; Reference number: S05050; MUID:89295563; PMID:2544807
A; Accession: S05051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-59 < ZELZ.)
A; Residues: 1-59 < ZELZ.)
A; Residues: 1-59 < ZELZ.)
A; Robert Siden Hertog, J.; van der Saag, P.T.; Kruijer, W. B; Shen, S.; Kruyt, F.A.E.; den Hertog, J.; van der Saag, P.T.; Kruijer, W. DNA Seq. 2, 111-119, 1991
A; Titler Mouse and human retinoic acid receptor beta-2 promoters: sequence comparison A; Reference number: $30489; MUID:92135889; PMID:1663808
A; Accession: $30490
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C;Superfamily: retinoic acid receptor alpha; erbA transforming protein homology
C;Keywords: alternative splicing; DNA binding; nucleus; transcription regulation; zi
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A:Molecule type: mRNA
A:Residues: 1-448 <ZEL1>
R:Zelent, 7.; Mendelsohn, C.; Kastner, P.; Krust, A.; Garnier, J.M.; Ruffenach, F.;
EMBO J. 10, 71-81, 1991
A;Title: Differentially expressed isoforms of the mouse retinoic acid receptor beta
A;Reference number: S13515; MUID:91114714; PMID:1846599
                                                                                                                                                                        295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           358 VRKRRPSRPHMFPKMLMKITDLRSISAKGAERVITLKMEIPGSMPPLIQEMLENSEGLDT 417
                                                                                                     56 TQSTSSEELVPSPPSPLPPPRVYKPCFVCQDKSSGYHYGVSACEGCKGFFRRSIQKNMIY
                                                                                                                                                                                                                                                                              356 IRKRRPSKPHWFPKILMKITDLRSISAKGAERVITLKMEIPGSMPPLIQEMLENSEGHEP
                                                                           TQSSSSEEIVPSPPSPPLPRIYKPCFVCQDKSSGYHYGVSACEGCKGFFRRSIQKNMVY
                                                                                                                                                                                                                                                                                                                                                                                    AKQLPGFTTLTIADQITLLKAACLDILILRICTRYTPEQDTMTFSDGLTLNRTQMHNAGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72.7%; Score 1771; DB 2;
74.8%; Pred. No. 1.7e-122;
tive 40; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              418 LSGQPGGGGRDGGGLPPPPGSCSPSLSPSSNRSSPATHSP
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R;Dejean, A.; de The, H.
Mol. Biol. Med. 7, 213-222, 1990
A;Title: Hepatitis B virus as an insertional mutagene in a human hepatocellular carcinom A;Reference number: 157458; MUID:91014673; PMID:2170809
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C;Reywords: alternative splicing; DNA binding; nucleus; transcription regulation; zinc
F;79-330/Domain: erba transforming protein homology <ERBA>
F;81-101/Region: zinc finger
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A; Residues: 1-406, M', 408-448 <DET>
A; Residues: 1-406, M', 408-448 <DET>
A; Cross-references: GB:Y00291
A; Experimental source: liver
R; Shen, S.; Kruyt, F.A.E.; den Hertog, J.; van der Saag, P.T.; Kruijer, W.
By Seq. 2, 111-119, 1991
A; Title: Mouse and human retinoic acid receptor beta-2 promoters: sequence comparison
A; Reference number: $30489; MUID:92135889; PMID:1663808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hepatocellular carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N.Alternate names: thyroid hormone receptor related protein
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Aug-1999
C.Accession: 802827; A2942; S30489; IS7458
R.Benbrook, D.; Lernhardt, E.; Pfahl, M.
Nature 333, 669-672, 1988
A.Title: A new retinoic acid receptor identified from a hepatocellular carcinoma A.Reference number: 802827; MUID:88232961; PMID:2836738
A.Reference number: 802827; MUID:88232961; PMID:2836738
A.Status: nucleic acid sequence not shown
A.Residues: 14-48 CABIN.
A.Status: nucleic acid sequence not shown
A.Residues: 14-48 CABIN.
A.Accession: 8028-7
A.Accession: 8028-7
A.Accession: 8028-7
A.Accession: 8028-7
A.Accession: 8028-802; MUID:88065931; PMID:2825037
A.Accession: A29492; MUID:88065931; PMID:2825037
A.Accession: 8028-802
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                        295
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A; Residues: 54-102 <RES>
A; Cross-references: GB:M57445; NID:9184476; PIDN:AAA58728.1; PID:9184477
                                                                                                                   GFGPLTDLVFAFANQLLPLEMDDAETGLLSAICLICGDRQDLEQPDRVDMLQEPLLEALK
                                                                                                                                           EFAKQLPGFTTLTIADQITLLKAACLDILILRICTRYTPEQDTMTFSDGLTLNRTQMHNA
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74.8%; Pred. No. 4.5e-123;
tive 41; Mismatches 57;
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A; Residues: 1-52 <SHE>
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                336
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1 MYESVEVGGPTPNPFLVVDFYNQN-RACLLPEKGLPAPGPYSTPLRTPLWNGSN--HSIE

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1 MYESVEVGGPTPNPFLVVDFYNQN-RACLLPEKGLPAPGPYSTPLRTPLWNGSN--HSIE 57

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retinoic acid binding protein-
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A Residues: 1-455 < PAD>
A Cross-references: EMBL:X56674; NID:g63785; PIDN:CAA39997.1; PID:g63786
A Cross-references: EMBL:X56674; NID:g63785; PIDN:CAA39997.1; PID:g63786
A Note: the nuclectide sequence was submitted to the EMBL Data Library, November 1
B Nohno, T.; Muto, K.; Noji, S.; Saito, T.; Taniguchi, S.
B Hochim. Biophys. Acta 1089, 273-275, 1991
A; Title: Isoforms of retinoic acid receptor beta expressed in the chicken embryo.
A; Reference number: S16243; MuID:91274365; PMID:1647216
A; Accession: S17073
A; Molecule type: mRNA
A; Residues: 1-29, 'P', 31-80 < NOH>
C; Superfamily: retinoic acid receptor alpha; erbA transforming protein homology
C; Keywords: alternative splicing; DNA binding; nucleus; transcription regulation;
                                                                                                                               protein homology
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C;Species: Gallus gallus (chicken)
C;Date: 21-Nov-1993 #sequence_revision 22-Apr-1995 #text_change 15-Oct-1999
C;Accession: S13512; S17073
C;Accession: S13512; Moleod, L.B.; Suzuki, H.; Solursh, M.
Nucleic Acids Res. 19, 395, 1991
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                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                        1 MYESVEVGGPTPNPFLVVDFYNQN-RACLLPEKGLPAPGPYSTPLRTPLW--NGSNHSIE
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A;Aeference number: S13512; MUID:91195065; PMID:1849630
A;Accession: S13512
A;Status: nucleic acid sequence not shown; translation not shown
                                                                                                                               erbA transforming
                            A Accession: S16243
A: Molecule type: mRNA
A: Molecule type: mRNA
A: Residues: 15-60
A: COSS-references: EMBL:X57339
C; Superfamily: retinoic acid receptor alpha; erbA transform
C; Seywords: alternative splicing; DNA binding; zinc finger
F; 79-330/Domain: erbA transforming protein homology <ERBA>
F; 81-101/Region: zinc finger
F; 117-141/Region: zinc finger
number: $16243; MUID:91274365; PMID:1647216
: $16243
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; Pred. No. 1.9e-121;
42; Mismatches 58;
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A; Residues: 1-448 <SMI>
A; Cross-references: GB:X59473; NID:g63753; PIDN:CAA42077.1; PID:g63754
A; Note: the authors translated the codon ACT for residue 96 as Ser, TCC for residue 167
R; Noj1, S.; Nohno, T.; Koyama, E.; Muto, K.; Ohyama, K.; Aoki, Y.; Tamura, K.; Ohsugi, R
Nature 350, 83-86, 1991
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A;Accession: S14291
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A; Residues: 1-95, 'S', 97-448 <NOJ>
A; Cross-references: EMBL:X57340; NID:g62976; PIDN:CAA40616.1; PID:g62977
A; Rowe, A.; Richman, J.M.; Brickell, P.M.
Development 111, 1007-1016, 1991
Development Entinoic acid treatment alters the distribution of retinoic acid receptor-beta
A; Reference number: A60129; MUID:91347912; PMID:1652423
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A; Residues: 15-95, 'S', 97-434 <NOH1>
A; Cross-references: EMBL:357339
R; Nohno, T.; Muto, K.; Noli, S.; Salto, T.; Taniguchi, S.
Biochim. Biophys. Acta 1089, 273-275, 1991
A; Title: Isoforms of retinoic acid receptor beta expressed in the chicken embryo.
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C; Species: Gallus gallus (chicken)
C; Sate: 11-Dec-1992 #sequence_revision 30-Jan-1993 #text_change 20-Aug-1999
C; Accession: A47386; S14291; A60129; S17072; S16243
R; Smith, S.M.; Eichele, G.
Bovelopment 111, 245-525, 1991
A; Title: Temporal and regional differences in the expression pattern of distA; Reference number: A43786; MUID:91199956; PMID:1849811
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                                                                                                                                                                                                                                                                               178 EVGELIEKVRKAHQETFPALCQLGKYTTNNSSEQRVSLDIDLWDKFSELSTKCIIKTVEF 237
                                                                                                                                                                                                                                                                                                                                                                                        297
                                                                              TQSSSSEEIVPSPPSPPPLPRIYKPCFVCQDKSSGYHYGVSACEGCKGFFRRSIQKNMVY 117
     A;Molecule type: mRNA
A;Residues: 23-24,26-95,'S',97-165,'D',167-448 <ROW>
A;Cross-references: GB:S63196; NID:g234370; PIDN:AAB19628.1; PID:g234371
                                                                                                                                                                                                                                                                                                                                                                                     238 AKQLPGFTTLTIADQITLLKAACLDILILRICTRYTPEQDTMTFSDGLTLNRTQMHNAGF
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A;Reference number: S17072
A;Accession: S17072
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CHRDKNCIINKVTRNPCQYCRLQKCFEVGMSKESVRNDRNKKKKEVPKPEC--SESYTLT 176
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C;Species: Brachydanio renio (zebra fish)
C;Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 20-Aug-1999
C;Accession: 151257
R;Joore, J; van der Lans, G.B.; Lanser, P.H.; Vervaart, J.M.; Zivkovic, D.; Speksnijder
Mech. Dev. 46, 137-150, 1994
A;Title: Effects of retinoic acid on the expression of retinoic acid receptors during ze
A;Reference number: 151256; MUID:95001557; PMID:7918098
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C;Superfamily: retinoic acid receptor alpha; erbA transforming protein homology
F;75-327/Domain: erbA transforming protein homology <ERBA>
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F;86-337/Domain: erbA transforming protein homology <ERBA>F;88-108/Region: zinc finger
F;124-148/Region: zinc finger
                                                             Query Match
71.1%; Score 1733; DB 2;
Best Local Similarity 77.1%; Pred. No. 1.1e-119;
Matches 330; Conservative 33; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tch 68.3%; Score 1663.5; DB 2; al Similarity 71.3%; Pred. No. 1.6e-114; 328; Conservative 37; Mismatches 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-499 <JOO>
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NSSVSQSP 452
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Best Local S
Matches 328
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PEVGELIEKVRKAHQETFPALCQLGKYTTNNSSEQRVSLDIDLWDKFSELSTKCIIKTVE
                                                                                                            FAKOLPGFTTLTIADQITLLKAACLDILILRICTRYTPEQDTMTFSDGLTLNRTQMHNAG
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Search completed: March 29, 2003, 09:43:58 Job time : 37 secs

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GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

March 29, 2003, 06:37:58 ; Search time 24 Seconds
 (without alignments)
560.261 Million cell updates/sec Run on:

US-09-691-220-2 2437 1 MYESVEVGGPTPNPFLVVDF......SCSPSLSPSSNRSSPATHSP 457

Title: Perfect score:

Scoring table: Seguence:

262574 seqs, 29422922 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

262574 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued_Patents_AA:* Database :

/cgn2_6/ptodata/1/laa/5A_COMB.pep:*
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/cgn2_6/ptodata/1/laa/6A_COMB.pep:*
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/cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:* 4.0.0

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 2, Appli	4	4	4	4	7	7		4	Patent No. 5223606	Sequence 5, Appli	Sequence 5, Appli			Sequence 1, Appli		7	7	Patent No. 5438126	Sequence 3, Appli	'n			9	'n	~	Sequence 2, Appli
SUMMAKIES	ID	US-08-592-383-2	US-08-095-728B-4	PCT-US92-02320A-4	US-08-764-870-4	US-08-980-115-4	US-08-095-728B-2	PCT-US92-02320A-2	5171671-2	US-08-592-383-4	5223606-2	6	US-08-980-115-5	5260432-2	5223606-3	US-08-764-870-1	US-08-980-115-1	US-08-764-870-2	US-08-980-115-2	5438126-2	US-08-764-870-3	US-08-980-115-3	5223606-4	US-08-336-408B-6	PCT-US91-00399-6	US-08-342-411A-2	US-08-330-518-2	US-08-330-283-2
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	Score	2127	2127	2127	2114	2114	2112	2112	2111	1816	1777	1662	1662	1662	1625	658	658	652	652	652	O.	619.5	611	570	570	562	260	260
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US-08-646-248-2 PCT-US95-13924-2 PCT-US95-13931-2 US-08-373-935-1	US-08-333-358-8 US-08-463-694-8 US-08-684-501-8 US-08-776-844-2 US-08-775-652-3	PCT-US95-16311-3 US-08-342-411A-4 US-08-764-870-7 US-08-980-115-7	US-07-952-800-2 US-07-952-800-4 US-08-336-408B-2 US-08-764-870-6 US-08-980-115-6
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28 29 30		0 8 8 8 4 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0	44444

ALIGNMENTS

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GENERAL INFORMATION:
APPLICAMY: Tsai, S. and S.J. Collins
TITLE OF INVENTION: "Hematopoietic Cell Lines Bearing Altered Retinoic Acid Rec
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 462;
                                                                                                                                                                                                      ADDRESSEE: Christensen, O'Connor, Johnson and Kindness STREET: 2800 Pacific First Centre, 1420 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/099,242
FILING DATE: July 28, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Broderick, Thomas F.
REGISTRATION NUMBER: 31,332
REFERENCE/DOCKET NUMBER: FHCR-1-7190
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 1-206-682-8100; 1-206-224-0709(direct)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: polypeptide DESCRIPTION: sequence encoded by SEQ. ID. NO. 1
                                                                                                                                                                                                                                                                                                                                                  COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette-5.25 inch, 1.2Mb storage
COMPUTER: TBM PC/386 Compatible
OPPRATING SYSTEM: MS-DOS 4.01
SOFTWARE: Word for Windows 5.01-t
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/08/592,383
FILIG DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87.3%; Score 2127; DB 2;
91.6%; Pred. No. 1.3e-189;
tive 5; Mismatches 13;
                       Sequence 2, Application US/08592383 Patent No. 5830760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 462 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 91.65
Matches 413; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                             STATE: Washington COUNTRY: USA
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CITY: Seattle
STATE: Washingt
-08-592-383-2
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32 LGGLSP-PGALTTLOHQ------LPVSG-YSTP-----SPATIETQSSSSEEI 71

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VPSPPSPPPLPRIYKPCFVCQDKSSGYHYGVSACEGCKGFFRRSIQKNMVYTCHRDKNCI 126
                    12 VPSPPSPPPLPRIYKPCFVCQDKSSGYHYGVSACEGCKGFFRRSIQKNMVYTCHRDKNCI 131
                                                                          127 INKVTRNPCQYCRLQKCFEVGMSKESVRNDRNKKKKEVPKPECSESYTLTPEVGELIEKV 186
                                                                                                  192 RKAHQETFPALCQLGKYTTNNSSEQRVSLDIDLWDKFSELSTKCIIKTVEFAKQLFGFFT 251
                                                                                                                                                                                                                                    LTIADQITLLKAACLDILILRICTRYTPEQDTMTFSDGLTLNRTQMHNAGFGPLTDLVFA 306
                                                                                                                                                                                                                                                          FANQLLPLEMDDAETGLLSAICLICGDRODLEQPDRVDMLQEPLLEALKVYVRKRRPSRP 366
                                                                                                                                                                                                                                                                                                                                   426
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Patent No. 5843642
GENERAL INFORMATION:
APPLICANT: DMITROVSKY, ETHAN
APPLICANT: MILLER JR, MILSON H
APPLICANT: MILLER JR, WILSON H
APPLICANT: FRANKEL, STANLEY
TITLE OF INVENTION: TREATMENT OF ACUTE PROMYELOCYTIC LEUKEMIA (APL)
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                        187 RKAHQETFPALCQLGKYTTNNSSEQRVSLDIDLWDKFSELSTKCIIKTVEFAKQLPGFTT
                                                                                                                                                                                                                                                                                                                                                                                           HMFPKMLMKITDLRSISAKGAERVITLKMEIPGSMPPLIQEMLENSEGLDTLSGQPGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/095,728B
FILING DATE: 21-UL-1993
CLASSIFICATION: 435
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/673,838
FILING DATE: 22-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WHITE, JOHN P
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 38694-A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 462 amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : COOPER & DUNHAM LLP
1185 AVENUE OF THE AMERICAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: NEW YORK STATE: NEW YORK COUNTRY: U.S.A. ZIP: 10036
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US-08-095-728B-4
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CITY: NE
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67 VPSPPSPPPLPRIYKPCFVCQDKSSGYHYGVSACEGCKGFFRRSIQKNMVYTCHRDKNCI 126
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                                                                                                                                                                                                                                                                                               LTIADQITLLKAACLDILILRICTRYTPEQDTMTFSDGLTLNRTQMHNAGFGPLTDLVFA 306
                                                                                           Gaps
                                                                                                                            7 VGGPTPNPFLVVDFYNQNRACLLPEKGLPAPGPYSTPLRTPLWNGSNHSIETQSSSSEEI 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application PC/TUS9202320A
Sequence 4, Application PC/TUS9202320A
Sequence 4, Application PC/TUS9202320A
Sequence 5 Sequence:
APPLICANT: Sloan-Kettering Institute, For Cancer Research
TITLE OF INVENTION: METHODS FOR DETECTION AND TREATMENT OF CANCER NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & DUNHAM
STREET: 30 ROCKEFELLER PLAZA
CITY: NEW YORK
STATE: NEW YORK
CUTY: U.S.A.
                                                                                                                                                 32 LGGLSP-PGALTTLQHQ------LPVSG-YSTP-----SPATIETQSSSSEEI
                                                                                                                                                                                                                        12 VPSPPSPPPLPRIYKPCFVCQDKSSGYHYGVSACEGCKGFFRRSIQKNMYYTCHRDKNCI
                                                                                                                                                                                                                                                                                                                                                                       FANQLLPLEMDDAETGLLSAICLICGDRQDLEQPDRVDMLQEPLLEALKVYVRKRRPSRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HMFPKMLMKITDLRSISAKGAERVITLKMEIPGSMPPLIQEMLENSEGLDTLSGQPGGGG
                                                                                         20;
                                                                                        Indels
                                                   Score 2127; DB 2;
Pred. No. 1.3e-189;
5; Mismatches 13;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/02320A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RECISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 38694-PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: US 675,084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 22-WAR-1991
PRIOR APPLICATION DATA:
APPLICATION NOMBER: US 673
FILING DATE: 22-WAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WHITE, JOHN PREGISTRATION NUMBER: 28,67
                                                   87.3%;
                                                   Query Match 87.3:
Best Local Similarity 91.6:
Matches 413; Conservative
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
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US-08-095-728B-4
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TOPOLOGY: linear
MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                            127 INKVTRNPCQYCRLQKCFEVGMSKESVRNDRNKKKKEVPKPECSESYTLTPEVGELIEKV 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HMFPKMLMKITDLRSISAKGAERVITLKMEIPGSMPPLIQEMLENSEGLDTLSGQPGGGG 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                               32 IGGLSP-PGALTTLOHQ-------LPVSG-YSTP-----SPATIETQSSSSEEI 71
                                                                                                                                                                                                                                                             7 VGGPTPNPFLVVDFYNQNRACLLPEKGLPAPGPYSTPLRTPLWNGSNHSIETQSSSSEEI 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20;
                                                                                                                                                                                                    Length 462;
                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Nuclear Receptor Ligands and Ligand TITLE OF INVENTION: Binding Domains NUMBER OF SEQUENCES: 16 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Cooley Godward
STREET: Five Palo Alto Square, 3000 El Camino Real
                                                                                                                                                                                               Score 2127; DB 5;
Pred. No. 1.3e-189;
5; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RDGGGLPPPPGSCSPSLSPSSNRSSPATHSP 457
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APPLICANT: Baxter, John D
APPLICANT: Fletterlick, Robert J
APPLICANT: Wagner, Richard L
APPLICANT: Kushner, Perer J
APPLICANT: Apriletti, James W
APPLICANT: West, Brian
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 644-0525
TELEX: (212) 42523 COOP UI
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 462 mmino acids
TYPE: amino acids
TYPE: amino acids
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/08764870 Patent No. 6236946
                                                                                                                                                                                             Query Match 87.3%;
Best Local Similarity 91.6%;
Matches 413; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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104 KGFFRRSIQKNMVYTCHRDKNCIINKVTRNPCQYCRLQKCFEVGMSKESVRNDRNKKKKE 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           344 DMLQEPLLEALKVYVRKRRPSRPHMFPKMIMKITDLRSISAKGAERVITLKMEIPGSMPP 403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 KGFFRRSIQKNMVYTCHRDKNCIINKVTRNRCQYCRLQKCFEVGMSKESVRNDRNKKKKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 164 VPKPECSESYTLTPEVGELIEKVRKAHQETFPALCQLGKYTTNNSSEQRVSLDIDLWDKF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNMER: US/08/764,870
FILING DATE: 13-DEC-1996
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 2114; DB 4;
Pred. No. 1.8e-188;
2; Mismatches 2;
                                                                                                                                                      PULCATION: 330
PRICATION NUMBER: US 60/008,540
FILING DATE: 13-DEC-1995
FILING DATE: 13-DEC-1995
PRICATION NUMBER: US 60/008,543
APPLICATION DATA: ADELICATION DATA: APPLICATION NUMBER: US 60/008,606
FILING DATE: 14-DEC-1995
ATTORNEY AGENT INFORMATION:
NAME: Nakamura, Jackie N
REGISTATION NUMBER: 35,966
RECISTATION NUMBER: 35,966
RECISTATION NUMBER: 35,966
RELECHONE: (650)843-5000
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/08980115; Patent No. 626622; GENERAL INFORMATION: APPLICANT: Scanlan, Thomas S.; APPLICANT: Baxter, John D.; APPLICANT: Fletterick, Robert J.; APPLICANT: Wagner, Richard L.
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Best Local Similarity 97.1%;
Matches 402; Conservative
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CORRESPONDENCE ADDRESS:
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                                                                APPLICANT: Shidu, Andrew K.

TITLE OF INVENTION: NUCLEAR RECEPTOR LIGANDS AND LIGAND BINDING DOMAINS
FILE REFERENCE: CCAL-246/02US
CURRENT APPLICATION NUMBER: US/08/980,115
CURRENT FILING DATE: 1997-11-26
EARLIER PEDLICATION NUMBER: 08/764,870
EARLIER FILING DATE: 1996-12-13
EARLIER FILING DATE: 1995-12-14
EARLIER PELICATION NUMBER: 60/008,606
EARLIER FILING DATE: 1995-12-13
EARLIER FILING DATE: 1995-12-13
EARLIER FILING DATE: 1995-12-13
SOFTWARE: PAPPLICATION NUMBER: 60/008,540
EARLIER FILING DATE: 1995-12-13
SOFTWARE: PAPPLICATION NUMBER: 60/008,540
EARLIER FILING DATE: 1995-12-13
SOFTWARE: PAPPLICATION NUMBER: 60/008,540
EARLIER PILING DATE: 1995-12-13
SOFTWARE: PAPPLICATION NUMBER: 60/008,540
EARLIER FILING DATE: 1995-12-13
SOFTWARE: PAPPLICATION NUMBER: 60/008,540
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Patent No. 5843642
GENERAL INFORMATION:
APPLICANT: DMITROVSKY, ETHAN
APPLICANT: WARRELL JR, WILSON H
APPLICANT: MILLER JR, WILSON H
APPLICANT: MILLER JR, WILSON H
APPLICANT: METHODS FOR THE DETECTION AND
TITLE OF INVENTION: METHODS FOR THE DETECTION AND
TITLE OF INVENTION: TREATMENT OF ACUTE PROMYELOCYTIC LEUKEMIA (APL)
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                164 VPKPECSESYTLTPEVGELIEKVRKAHQETFPALCQLGKYTTNNSSEQRVSLDIDLWDKF
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Best Local Similarity 97.1%; Pred. No. 1.8e-188;
Matches 402; Conservative 2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY: DOMAIN
; LOCATION: (131)..(373)
; CTHER INFORMATION: minimal ligand binding domain
US-08-980-115-4
APPLICANT: Kushner, Peter J.
APPLICANT: Apriletti, James W.
APPLICANT: West, Brian L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-095-728B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
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55 SIETQSSSSEEIVPSPPSPPPLPRIYKPCFVCQDKSSGYHYGVSACEGCKGFFRRSIQKN 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  175 LTPEVGELIEKVRKAHQETFPALCQLGKYTTNNSSEQRVSLDIDLWDKFSELSTKCIIKT 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGFGPLTDLVFAFANQLLPLEMDDAETGLLSAICLICGDRQDLEQPDRVDMLQEPLLEAL 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        635 AGFGPLTDLVFAFANQLLPLEMDDAETGLLSAICLICGDRQDLEQPDRVDMLQEPLLEAL 694
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TITLE OF INVENTION: METHODS FOR DETECTION AND TREATMENT OF CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VEFAKQLPGFTTLTIADQITLLKAACLDILILRICTRYTPEQDTMTFSDGLTLNRTQMHN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; DB 2;
6.9e-188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 2112; DB
Pred. No. 6.9e-
1; Mismatches
                                                                                                                         COMPUTER READABLE FUKM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELease #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/095,728B
FILING DATE: 21-JUL-1993
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/673,838
FILING DATE: 22-MAR-1991
APPLICATION NUMBER: 28,678
FILING DATE: 22-MAR-1991
APPLICATION NUMBER: 28,678
FILING DATE: 10HN P
REGISTRATION NUMBER: 38694-A
TELECHONORICATION INFORMATION:
TELECHONE: (212) 278-0400
TELECHONE: (212) 391-0525
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGRIF APILO ACID
: COOPER & DUNHAM LLP
1185 AVENUE OF THE AMERICAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application PC/TUS9202320A
GENERAL INFORMATION:
APPLICANT: Sloan-Kettering Institut
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                                                                                COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 400; Conservat
                                                                    NEW YORK
                                         CITY: NEW YORK STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCT-US92-02320A-2
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Matches 411; Conservative
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               5171671
                                                                                                                                                                                                              LENGTH: 462
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                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                  ;SEQ ID NO:2
  5171671-2; Patent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LTPEVGELIEKVRKAHQETFPALCQLGKYTTNNSSEQRVSLDIDLWDKFSELSTKCIIKT 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VEFAKQLPGFTTLTIADQITLLKAACLDILILRICTRYTPEQDTMTFSDGLTLNRTQMHN 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86.7%; Score 2112; DB 5; Length 797; 99.3%; Pred. No. 6.9e-188; tive 1; Mismatches 2; Indels
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                                                                                                                                                                                 APPLICATION NUMBER: PCT/US92/02320A
                                                                                                                                                                                            FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
CLING DATE: 22-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0S 673,838
FILING DATE: 22-MAR-1991
ATTONNEY/AGENT INFORMATION:
NAME: WHITE, JOHN P
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 28,678
RESERENCE/DOCKET NUMBER: 38694-PC
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                      SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
                       ADDRESSEE: COOPER & DUNHAM
STREET: 30 ROCKEFELLER PLAZA
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
                                                                                     ZIF: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                       (212) 644-0525
(212) 422523 COOP UI
                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 797 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
             CORRESPONDENCE ADDRESS:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 400; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCT-US92-02320A-2
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RESULT 8

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Sequence 4, Application US/08592383
Patent No. 5830760
GENERAL INFORMATION:
APPLICANT: Tsai, S. and S.J. Collins
TITLE OF INVENTION: "Hematopoietic Cell Lines Bearing Altered Retinoic Acid Rec
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67 VPSPPSPPPLPRIYKPCFVCQDKSSGYHYGVSACEGCKGFFRRSIQKNMVYTCHRDKNCI 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      127 INKVTRNPCQYCRLQKCFEVGMSKESVRNDRNKKKKEVPKPECSESYTLTPEVGELIEKV 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             247 LTIADQITLLKAACLDILILRRICTRYTPEQDTMTFSDGLTLNRTQMHNAGFGPLTDLVFA 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 VGGPTPNPFLVVDFYNQNRACLLPEKGLPAPGPYSTPLRTPLWNGSNHSIETQSSSSEEI 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32 LGGLSP-PGALTTLQHQ------LPVSG-YSTP-----SPATIETQSSSSEEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RKAHQETFPALCQLGKYTTNNSSEQRVSLDIDLWDKFSELSTKCIIKTVEFAKQLPGFTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 462;
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STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                 TITLE OF INVENTION: RETINOIC ACID RECEPTOR COMPOSITION NUMBER OF SEQUENCES: 2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/546,256
FILING DATE: 06-AUG-1990.
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 276,536
FILING DATE: 30-NOV-1988
APPLICATION NUMBER: 126,331
FILING DATE: 02-DEC-1987
; APPLICANT: EVANS, RONALD M.;ONG, ESTELITA S.;SEGUI,;PRUDIMAR S.;THOMPSON, CATHERINE C.;UEMSONO, KAZUHIKO;GUGUERE, VINCENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Diskette-5.25 inch, 1.2Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                86.6%; Score 2111; DB 6;
91.1%; Pred. No. 3.9e-188;
iive 5; Mismatches 15;
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us-09-691-220-2.rai

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COMPUTER READABLE FORM:
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                                                            Matches 343;
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                                Query Match
Best Local 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                127 INKVTRNPCQYCRLQKCFEVGMSKESVRNDRNKKKKEVPKPECSESYTLTPEVGELIEKV 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                           7 VGGPTPNPFLVVDFYNQNRACLLPEKGLPAPGPYSTPLRTPLWNGSNHSIETQSSSSEEI 66
                                                                                                                                                                                                                                                                                                                                                                                                                                           RKAHQETFPALCQLGKYTTNNSSEQRVSLDIDLWDKFSELSTKCIIKTVEFAKQLPGFTT
                                                                                                                                                                                                                                                                                                                              3; RAR-alpha403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: STEROID/THYROID HORMONE RECEPTOR-RELATED PROPROPERIOR IN THE SECURITY EXPRESSED IN HUMAN HEPATOCELLULAR CARCINOMA NUMBER OF SEQUENCES: 11 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                   20;
                                                                                                                                                                                                                                                                                                                                                                         Length 403;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Patent No. 5223606
; APPLICANT: BLAUDIN DE THE, HUGHES; MARCHIO, AGNES; TIOLLAIS,
; PIERRE; DEJEAN, ANNE
                                                                                                                                                                                                                                                                                                                                                                    Score 1816; DB 2; Length 40
Pred. No. 9e-161;
5; Mismatches 12; Indels
                                                                                        PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/099,242

FILING DATE: July 28, 1993

ATTORNEY/ADENT INFORMATION:

NAME: Broderick, Thomas F.

REGISTRATION NUMBER: 31,332

REGISTRATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION NO: 4:

TELECOMMUNICATION NO: 4:

FROME ENAMATION FOR SEQ ID NO: 4:

FROME CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: polypeptide DESCRIPTION: sequence encoded by SEQ. ID. NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HMFPKMLMKITDLRSISAKGAERVITLKMEIP 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for Windows 5.01-t
                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/07/134,130 FILING DATE: 17-DEC-1987 PRIOR APPLICATION DATA: ID NO.2: LENGTH: 448
COMPUTER: IBM PC/386 Compatible OPERATING SYSTEM: MS-DOS 4.01
                                                                                                                                                                                                                                                                                                                                                                   Query Match 74.5%;
Best Local Similarity 90.6%;
Matches 355; Conservative
                                                                                                                                                                                                                                                         403 amino acids
                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                  CLASSIFICATION: 435
                             Word
                                                                   FILING DATE:
                            SOFTWARE
                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                        US-08-592-383-4
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58 TQSSSSEEIVPSPPSPPPLPRIYKPCFVCQDKSSGYHYGVSACEGCKGFFRRSIQKNMVY 117
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                                                                                                                                                                                                                                                                  Gaps
                                                                                                     1 MYESVEVGGPTPNPFLVVDFYNQN-RACLLPEKGLPAPGPYSTPLRTPLWNGSN--HSIE 57
                                                                                                                                                                                                                                                                                                                                                EVGELIEKVRKAHQETFPALCQLGKYTTNNSSEQRVSLDIDLWDKFSELSTKCIIKTVEF
                                                                                                                                                                                                                                                                                                                                                                                                          AKQLPGFTTLTIADQITLLKAACLDILILRICTRYTPEQDTMTFSDGLTLNRTQMHNAGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        358 VRKRRPSRPHMFPKMLMKITDLRSISAKGAERVITLKMEIPGSMPPLIQEMLENSEGLDT
                                          18;
                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Nuclear Receptor Ligands and Ligand TITLE OF INVENTION: Binding Domains NUMBER OF SEQUENCES: 16 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3000 El Camino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       418 LSGQPGGGGRDGGGLPPPGSCSPSLSPSSNRSSPATHSP 457
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  7; DB 6;
4.5e-157;
Score 1777; DE
Pred. No. 4.5e-
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/008,540
FILING DATE: 13-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/764,870
FILING DATE: 13-DEC-1996
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 5, Application US/08764870; Patent No. 6236946; GENERAL INFORMATION: APPLICANT: Scanlan, Thomas S APPLICANT: Baxter, John D APPLICANT: Fletterick, Robert J APPLICANT: Wagner, Richard L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Cooley Godward
STREET: Five Palo Alto Square,
CITY: Palo Alto
STATE: CA
                                        42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Kushner, Peter J
APPLICANT: Apriletti, James W
APPLICANT: West, Brian
  72.98;
                       74.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
                                          Conservative
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LENGTH: 454
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GENERAL INFORMATION:
APPLICANT: Scanlan, Thomas S.
APPLICANT: Baxter, John D.
APPLICANT: Hetterick, Robert J.
APPLICANT: Wagner, Richard L.
APPLICANT: Manner, Peter J.
APPLICANT: Mest, Brian L.
APPLICANT: Mest, Brian L.
APPLICANT: Shian L.
APPLICANT: Shian L.
APPLICANT: SHIAN ANCHEW K.
TITLE OF INVENTION: NUCLEAR RECEPTOR LIGANDS AND LIGAND BINDING DOMAINS FILE REFERENCE: UCAL-246/02US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KVTRNPCQYCRLQKCFEVGMSKESVRNDRNKKKKEVPKPECSESYTLTPEVGELIEKVRK 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPPSPPPLPRIYKPCFVCQDKSSGTHYGVSACEGCKGFFRRSIQKNMVYTCHRDKNCIIN 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSPSPPPPPRVYKPCFVCNDKSSGYHYGVSSCEGCKGFFRRSIQKNMYYTCHRDKNCIIN 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68.2%; Score 1662; DB 4; 72.8%; Pred. No. 2.3e-146; tive 39; Mismatches 48;
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/008,543
FILING DATE: 13-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/008,606
FILING DATE: 14-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: NAKENUMBER: 35,966
REGISTRATION NUMBER: 35,966
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFORMATION:
TELECOMMUNICATION INFORMATION INFORMATION INFORMAT
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Patent No. 6266622
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                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 454 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 72.89
Matches 319; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , MOLECULE TYPE: protein US-08-764-870-5
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US-08-980-115-5
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SPSPPPPPRVYKPCFVCNDKSSGYHYGVSSCEGCKGFFRRSIQKNMYYTCHRDKNCIIN 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          136 KVTRNRCQYCRLQKCFEVGMSKEAVRNDRNKKKKEVKEEGSPDSYELSPQLEELITKVSK 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           189 AHQETFPALCQLGKYTTNNSSEQRVSLDIDLWDKFSELSTKCIIKTVEFAKQLPGFTTLT 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     249 IADQITLLKAACLDILILRICTRYTPEQDTMTFSDGLTLNRTQMHNAGFGPLTDLVFAFA 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPPSPPPLPRIYKPCFVCQDKSSGYHYGVSACEGCKGFFRRSIQKNMVYTCHRDKNCIIN 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16 PGSGYPGAGFPFAFPGALRGSPPFEMLSPSFRGLGQPDLPKEMASLSVETQSTSSEEMVP 75
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Patent No. 5260432
Patent No. 5260432
Patent Tarkaku, FUMIMARO; ISHIKAWA, TAKASHI; IMAWARI, MICHIO;
FEVANS, ROMALD M.; UMESONO, KAZUHIKO
TITLE OF INVENTION: HUMAN GAMMA RETINOIC ACID RECEPTOR DNA
NUMBER OF SEQUENCES: 4
CURRENT APPLICATION NUMBER: US/07/370,407
FILING DATE: 22-JUN-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : LOCATION: (179)...(421)
; OTHER INFORMATION: minimal ligand binding domain
US-08-980-115-5
                    CURRENT FILING DATE: 1997-11-26
EARLIER APPLICATION NUMBER: 087764,870
EARLIER PILING DATE: 1996-12-13
EARLIER PELLORATION NUMBER: 60/7008,606
EARLIER FILING DATE: 1995-12-14
EARLIER FILING DATE: 1995-12-14
EARLIER FILING DATE: 1995-12-13
EARLIER FILING DATE: 1995-12-13
EARLIER APPLICATION NUMBER: 60/7008,540
EARLIER FILING DATE: 1995-12-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PATENTIN VET: 2.0
APPLICATION NUMBER: US/08/980,115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             424 -----GGGRDGGGLPPP 435
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                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; SEQ ID NO:2:
; LENGTH: 454
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us-09-691-220-2.rai

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SAKGAERVITLKMEIPGSMPPLIQEMLENSEGLDTLSGQPGGGGRDGGGLPPPPGSCSPS 442
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                         LLSAICLICGDRQDLEQPDRVDMLQEPLLEALKVYVRKRRPSRPHMFPKMLMKITDLRSI
                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Nuclear Receptor Ligands and Ligand TITLE OF INVENTION: Binding Domains NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTE: FLORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,870
FILING DATE: 13-DEC-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/008,540
FILING DATE: 13-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/008,543
ATTENDO TO NUMBER: US 60/008,543
ATTENDO TO NUMBER: US 60/008,543
ATTENDO TO NUMBER: US 60/008,543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Cooley Godward
STREET: Five Palo Alto Square, 3000 El Camino
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38.1%; Pred. No. 5e-53;
1ve 64; Mismatches 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: NAKAMURA, Jackie N
REGISTRATION NUMBER: 35,966
REFERENCE/DOCKET NUMBER: UCAL-246/01US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 60/008,606
FILING DATE: 14-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 60/008,543
FILING DATE: 13-DEC-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                   Baxter, John D
Fletterick, Robert J
Wagner, Richard L
Kushner, Peter J
                                                                                                                                                                                                                                                                  Sequence 1, Application US/08764870 Patent No. 6236946
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Apriletti, James W. APPLICANT: West, Brian
                                                                                                                                                                                                                                                                                                                    Scanlan, Thomas S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (650)843-5000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 38.19
Matches 139; Conservative
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351 ISPSSVENSGVSQSP 365
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STATE: CA
                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
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                                                                                                                                   69 SPPSPPPLPRIYKPCFVCQDKSSGYHYGVSACEGCKGFFRRSIQKNMVYTCHRDKNCIIN 128
                                                                                                                                                                                                                              249 IADQITLLKAACLDILILRICTRYTPEQDTWTFSDGLTLNRTQMHNAGFGPLTDLVFAFA 308
                                                                                                                                                                                                                                                                                                                                                                309 NQLLPLEMDDAETGLLSAICLICGDRQDLEQPDRVDMLQEPLLEALKVYVRKRRPSRPHM 368
                                                                                                                                                                                                                                                                                                                                                                                                                                      369 FPKMLMKITDLRSISAKGAERVITLKMEIPGSMPPLIQEMLENSEGLDTLSGQPG---- 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KVTRNPCQYCRLQKCFEVGMSKESVRNDRNKKKKEVPKPECSESYTLTPEVGELIEKVRK 188
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                                                                  30 PEKGLPAPG-PYSTP------LRTPLWNG-----SNHSIETQSSSSEEIVP 68
                                                                                          16 PGSGYPGAGFPFAFPGALRGSPPFEMLSPSFRGLGQPDLPKEMASLSVETQSTSSEEMVP 75
                                                                                                                                                                                                                                                                                             RESULT 14
5223606
7 PAGE TO SECULT 14
PLEAR NO. 5223606
PIERE; DEJEANT: BLAUDIN DE THE, HUGHES; MARCHIO, AGNES; TIOLLAIS,
PIERRE; DEJEAN, ANNE
TITLE OF INVENTION: STEROID/THYROID HORMONE RECEPTOR-RELATED
PROTEIN INAPPROPERTES: 11
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/134,130
FILING DATE: 17-DEC-1987
PRIOR APPLICATION DATA:
SEQ ID NO:3:
                                     32;
     Length 454;
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                                     48; Indels
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 ; Score 1662; DB 6;
; Pred. No. 2.3e-146;
39; Mismatches 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 1625; DB 6;
; Pred. No. 4.6e-143;
27; Mismatches 32;
68.2%;
72.8%;
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81.6%;
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                                Matches 319; Conservative
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Best Local Similarity 81.6
Matches 306; Conservative
                  Similarity
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                  Best Local
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	405 FEDOE 409	405	Dp
	409 LENSE 413	409	Qy
404	345 YLLAFEHYVHRKHNIPHFWPKLLMKYTDLRMIGACHASRFLHMKVECPTELFPPLFLEV	345	đ
408	350 LLEALKVYVRKRRPSRPHMFPKMLMKITDLRSISAKGAERVITLKMEIPGSM-PPLIQEM 408	350	οy
344	KOLKNGGLGVVSDAIFELGKSLSAFNLDDTEVALLQAVLLMSTDRSGLLCVDKIEKSQEA 344	285	QQ
349	290 TOWHNAGFGPLTDLVFAFANQLLPLEMDDAETGLLSAICLICGDRQDLEQPDRVDMLQEP 349	290	QY
284	225 AITRVVDFAKKLPMFSELPCEDQIILLKGCCMEIMSLRAAVRYDPESDTLTLSGEMTVKR	225	qα
289	230 CIIKTVEFAKOLDGFTTLTIADQITTLKAACLDILILRICTRYTPEQDTWTFSDGLTLNR 289	230	Qy
224	165 WDLIHVATEAHRSTNAGGSHWKORRKFLPDDIGGSPIVSMPDGDKVDLEAFSEFTKIITP 224	165	đ
229		180	QY
164	KKCIAVGMAMDLVLDDSKRVAKRKLIEQNRERRRKEEMIRSLQQRPEPTPEE	113	qa
179	OKCFEVGMSKESVRNDRNKKKKEV	141	δ
112	:	23	අු

Search completed: March 29, 2003, 09:44:44 Job time: 26 secs

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MEL: 2602-426282/45.
N-PSDB; AAL38338, AAL38339.
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Retinoic acid rece
Ligand binding dom
Novel human diagno
Novel human diagno
Novel human diagno
myl/RAR-alpha fusi
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RAR-alpha, Homo s
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                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*
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:/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
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2437
1 MYESVEVGGTPNNFLVVDF.....SCSPSLSPSSNRSSPATHSP
GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                              908470 seqs, 133250620 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                         OM protein - protein search, using sw model
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AAP90395
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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Human myl/RAR-alph Novel human diagno Murine Retinoic Ac Novel human diagno Novel human diagno RAR-alpha-403 domi hap (hepatoma) pro Murine Retinoic Ac Murine Retinoic Ac Murine Retinoic Ac Human RAR-beta. H Human RAR-beta. H Human RAR-beta. H Human RAR-beta. Gerombinant human Human Retinoic aci Mouse retinoic aci Novel human diagno Human retinoic aci Skin-specific muri Ligand binding dom Novel human diagno Novel human diagno Sequence encode by Ligand binding dom Human retinoic aci Fragment of retino Sequence encode by Ligand binding dom Human retinoic aci	
AAW81963 ABG18860 AAR10547 AAR84724 AAR84724 AAR603049 AAR50304 AAR66764 AAR86710182 AAR8723 AAR84723 AAR84723 AAR84723 AAR84725 AAR84723 AAR84723 AAR84723 AAR84723 AAR8720465 AAR20465 AAR20465 AAR20465 AAR20465 AAR20465 AAR20465 AAR20465 AAR872335 AAR86316 AAR10549 AAR721629 AAR3162 AAR3162	AAW41493 AAY21630 AAY21631 AAR47621 AAR80921 AAR807683
10 5 5 2 7 7 5 6 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	19 20 20 15 11
7 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	410 4110 461 514 516 345
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2112 2012 2089 2089 2089 1932 1932 1932 1771 1771 1771 1760 1662 1662 1662 1662 1662 1662 1662 16	652 649 619.5 617 611 591.5
	0.44444 0.010043

ALIGNMENTS

Human nuclear hormone receptor; therapeutic agent; gene therapy; Beasley EM; Di Francesco V, Human nuclear hormone receptor protein. AAO21489 standard; Protein; 457 AA. Ketchum KA, 2001WO-US31095 11-OCT-2000 2000US-239117P (first entry) Ye J, Yan C, PEKE) FE CORP NY. immune response WO200231146-42 Homo sapiens. 15-AUG-2002 18-APR-2002. 05-0CI-2001; AA021489; Wei M, AA021489

New human nuclear hormone receptor proteins and nucleic acids, useful as models or targets for developing human therapeutic targets, and in

09-MAR-1993 (first entry)

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definition in a salve as a cargerator pure are transference to the salve as a cargerate to the salve as a cargerate to the salve as a cargerate to the salve as a query sequence to perform searches against sequence at 15sues that express the nuclear hormone receptor. The nucleic acids may be used as a query sequence to perform searches against sequence at tabases to identify family members or related sequences, as probes or primers, to construct recombinant vectors, to identify compounds that modulate nuclear hormone receptor nucleic acid expression, in gene therapy, and as antisense constructs to control nuclear hormone receptor gene expression in cells, tissues or organisms. The polypeptides can be cased to raise antibodies or to elicit an immune response, as a reagent in assays designed to determine protein levels in biological fluids, as markers for tissues in which a corresponding protein is expressed, to identify a binding partner/ligand to develop a system for the cidentification of inhibitors of the binding partner/ligand to assays, and to identify compounds that modulate protein activity. This sequence represents the human nuclear hormone receptor protein of the
                                                                                                                                                      The invention relates to an isolated peptide of a novel human nuclear hormone receptor with a fully defined sequence of 457 amino acids given in the specification. The novel human nuclear hormone receptor peptides and nucleic acids encoding them can be used as models for the development of human therapeutic targets, aid in the identification of therapeutic proteins, and serve as targets for the development of human therapeutic
      nuclear hormone
   identifying therapeutic proteins and modulators of
                                                                                          Claim 1; Fig 2; 73pp; English.
                                    receptor expression
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Length 457; Indels Score 2437; DB 23; Pred. No. 7.7e-201; Mismatches ó 100.0%; Matches 457; Conservative Query Match Best Local Similarity 457 AA; nvention. Sequence

ö SSSEEIVPSPPSPPPLPRIYKPCFVCQDKSSGYHYGVSACEGCKGFFRRSIQKNMVYTCH 120 ELIEKVRKAHQETFPALCQLGKYTTNNSSEQRVSLDIDLWDKFSELSTKCIIKTVEFAKQ 240 RDKNCIINKVTRNPCQYCRLQKCFEVGMSKESVRNDRNKKKKEVPRPECSESYTLTPEVG 180 LPGFTTLTIADQITLLKAACLDILILRICTRYTPEQDTMTFSDGLTLNRTQMHNAGFGPL 300 TDLVFAFANQLLPLEMDDAETGLLSAICLICGDRQDLEQPDRVDMLQEPLLEALKVYVRK 360 Gaps 9 9 MYESVEVGGPTPNPFLVVDFYNQNRACLLPEKGLPAPGPYSTPLRTPLWNGSNHSIETQS RRPSRPHMFPKMLMKITDLRSISARGAERVITLKMEIPGSMPPLIQEMLENSEGLDTLSG ö QPGGGGRDGGGLPPPPGSCSPSLSPSSNRSSPATHSP 457 -121 241 301 61 61 121 181 241 361 361 421 181 301 a ò 셤 ò g 셤 셤 셤 a ð ð ð õ õ ò

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Ā AAR27534 standard; Protein; 462 AAR27534; AAR27534

RESULT 2

421 QPGGGRDGGGLPPPPGSCSPSLSPSSNRSSPATHSP 457

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LTIADQITLLKAACLDILILRICTRYTPEQDIWTFSDGLTLNRTQWHNAGFGPLTDLVFA 306

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252 LTIADQITLLKAACLDILILRICTRYTPEQDIMTFSDGLTLNRTQMHNAGFGPLTDLVFA 311

FANQLLPLEMDDAETGLLSAICLICGDRQDLEQPDRVDMLQEPLLEALKVYVRKRRPSRP

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acid receptor (RAR)-alpha protein. The gene encoding this protein is disrupted in a translocation of a portion of the long arm of chromosome 17 (115:17)(q21;q11-22)]. This causes a fusion RAR-alpha and myl which is characteristic of acute promyelocytic leukemia (APL). The breakpoint region has been cloned and it has been shown that DNA rearrangements are clustered in the region of the first intron of RAR-alpha. This sequence was isolated by polymerase chain reaction (PCR). The primers used for amplification of this sequence can also be used to amplify the translocated region.
                                                                                                                    Retinoic acid receptor; RAR-alpha; myl; acute promyelocytic leukemia; APL; translocation; chromosome 17; chromosome 15; PCR; primer; [t(15;17)(q21;q11-22)]; breakpoint; polymerase chain reaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence given represents the amino acid sequence of the retinoic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 VGGPTPNPFLVVDFYNQNRACLLPEKGLPAPGPYSTPLRTPLWNGSNHSIETQSSSSEEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for acute promyelocytic leukaemia and other neoplasias ing nucleic acid and encoded abnormal retinoic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Miller WH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 462;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Evans RM, Frankel S, Kazizuka A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87.3%; Score 2127; DB 13;
91.6%; Pred. No. 3.5e-174;
iive 5; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 43-46; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SLOK ) SLOAN KETTERING INST CANCER.
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Matches 413; Conservative
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                                                        RAR-alpha protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dmitrovsky E,
                                                                                                                                                                                                                                                                                                                                                                                                                                              23-MAR-1992;
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22-MAR-1991;
                                                                                                                                                                                                                                                                                                               WO9216660-A.
                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Warrell RP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    comprising
                                                                                                                                                                                                                                                       Synthetic.
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LTIADQITLLKAAACLDILILRICTRYTPEQDTMTFSDGLTLNRTQMHNAGFGPLTDLVFA 306
                                                                             FANQLLPLEMDDAETGLLSAICLICGDRQDLEQPDRVDMLQEPLLEALKVYVRKRRPSRP 366
                                                                                                                                              HMFPKMLMKITDLRSISAKGAERVITLKMEIPGSMPPLIQEMLENSEGLDTLSGQPGGG 426
                                                                                                                                                                                                         truncation of sequences coding for the C-terminal 59 amino acids and part the 3' UTR of the wild-type human sequence (AAQ81476). This truncated cDNA, designated RAR-alpha-403, encodes a protein (AAR86024) containing the N-terminus, DNN-binding domain and part of the hormone-binding domain of RAR-alpha (AAR68023).
RKAHQETFPALCQLGKYTTNNSSEQRVSLDIDLWDKFSELSTKCIIKTVEFAKQLPGFTT
               retinoic acid receptor alpha; hematopoietic; stem cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 An RAR-alpha cDNA (given in AAQ81477) was prepared that contained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 VGGPTPNPFLVVDFYNQNRACLLPEKGLPAPGPYSTPLRTPLWNGSNHSIETQSSSSEEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New haematopoietic stem cell lines with specific differentiation properties - made by transfected stem cells with nucleic acid encoding dominant negative suppressor of the retinoic acid receptor alpha, useful e.g. for heematopoietic reconstitution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 2124; DB 16;
Pred. No. 6.4e-174;
6; Mismatches 13;
                                                                                                                                                                                                                                                                            RDGGGLPPPPGSCSPSLSPSSNRSSPATHSP 457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 56-58; 100pp; English.
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Matches 412; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W09504143-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Collins SJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RAR-alpha;
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187
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                       HMFPKMLMKITDLRSISAKGAERVITLKMEIPGSMPPLIQEMLENSEGLDTLSGQPGGGG 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VPSPPSPPPLPRIYKPCFVCQDKSSGYHYGVSACEGCKGFFRRSIQKNMVYTCHRDKNCI 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 VGGPTPNPFLVVDFYNQNRACLLPEKGLPAPGPYSTPLRTPLWNGSNHSIETQSSSSEEI 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32 LGGLSP-PGALTTLQHQ-------LPVSG-YSTP-----SPATIETQSSSSEEI 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Diagnosis of acute promyelocytic leukaemia - by detecting nucleic acid encoding abnormal retinoic acid receptor-alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20;
                                                                                                                                                                                                                                                                                                                   Fusion protein, myl; retinoic acid receptor-alpha; RAR; human; acute promyelocytic leukaemia; APL; t(15;17); translocation; treatment; all-trans retinoic acid.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 2127; DB 20;
Pred. No. 3.5e-174;
5; Mismatches 13;
                                                                                       Disclosure; Column 35-38; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SLOK ) SLOAN KETTERING INST CANCER RES
                                                                      RDGGGLPPPPGSCSPSLSPSSNRSSPATHSP
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                                                                                                                                                                                     AAW81964 standard; Protein; 462
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91.6%;
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91US-0673838.
91US-0675084.
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Best Local Similarity 91.6
Matches 413; Conservative
                                                                                                                                                                                                                                                                                      Human RAR-alpha protein.
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                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUL-1993;
22-MAR-1991;
                                                                                                                                                                                                                                                     05-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                    US5843642-A.
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                                                                                                                                                                                                                     AAW81964;
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                                      372
                                                                                                    432
      367
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                                                                                                                                                       RESULT
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4

Gaps 99

20;

Length 462; Indels

ð 셤 ò g à 硆 462 AA;

Sequence

So

4

Db 33 QQ 65 QQ 123 QQ 123 QQ 124 QQ 125 QQ 244 QQ 245 QQ 307 QQ 307 QQ 307 QQ 307 QQ 307 QQ 427 AAP90395 AAPP0395 AAPP03
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Thyroid hormone receptor; aromatic compound; ligand binding domain; alpha gloerophosphate dehydrogenase; cardiac; obesity; triglyceride; plasma cholesterol; anti-hypertriglyceridaemic; atherosclerosis; GPDH; thyroid hormone replacement therapy; nuclear receptor.
                                                                                        426
                                                                                                                                                                                   LTIADQITLLKAACLDILILRICTRYTPEQDTMTFSDGLTLNRTQMHNAGFGPLTDLVFA 306
                                                                                                                                                                                                                                              FANGLLPLEMDDAETGLLSAICLICGDRQDLEQPDRVDMLQEPLLEALKVYVRKRRPSRP 366
                                                                                                                                                                                                                                                                                           112 FANGLLPLEMDDAETGLLSAICLICGDRQDLEQPDRVDMLQEPLLEALKVYVRKRRPSRP 371
                                                                                                                                                                                                                                                                                                                                         Gaps
                                            7 VGGPTPNPFLVVDFYNQNRACLLPEKGLPAPGPYSTPLRTPLWNGSNHSIETQSSSSEEI 66
                                                          32 LGGLSP-PGALTILQHQ------LPVSG-YSTP------SPATIETQSSSSEEI 71
                                                                                                                                                                                                                                                                                                                              HMFPKMLMKITDLRSISAKGAERVITLKMEIPGSMPPLIQEMLENSEGLDTLSGQPGGG
                         20;
 Length 462;
                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kushner PJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ligand binding domain of nuclear receptor hRARalpha.
Query Match 87.0%; Score 2119; DB 10;
Best Local Similarity 91.4%; Pred. No. 1.7e-173;
Matches 412; Conservative 5; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modulating activity of a thyroid hormone receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JW, Baxter JD, Fletterick RJ, K
3, Shiau AK, Wagner RL, West BL;
                                                                                                                                                                                                                                                                                                                                                                                       RDGGGLAPPPGSCSPSLSPSSNRSSPATHSP 462
                                                                                                                                                                                                                                                                                                                                                                          RDGGGLPPPPGSCSPSLSPSSNRSSPATHSP 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY21636 standard; protein; 416 AA.
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Scanlan TS,
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23-AUG-2000; 2000US-0649167.

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                        The invention relates to a method for modulating activity of a thyroid which fits spatially and preferentially into a thyroid hormone ligand which fits spatially and preferentially into a thyroid hormone ligand binding domain. The aromatic compound (of a specified formula) can be used to increase alpha glecrophosphate dehydrogenase (GPDH) levels, at lavels which do not significantly modify cardiac GPDH levels and are indicated in the treatment of obesity. The compound also lower total blasma cholesterol and triglyceride levels and can be used as anti-hypertriglyceridaemic agents. The compound may also be used for treating thereozerosis and may be indicated in thyroid hormone replacement therapy in patients with compromised cardiac function. Sequences AAV21621-636 amino acid sequences of ligand binding domains of several members of the nuclear receptor superfamily.
                                                                                                                                                                                                                                                                                                                                                                                  SNH-----SIETQSSSSEEIVPSPPSPPPLPRIYKPCFVCQDKSSGYHYGVSACEGC 103
                                                                                                                                                                                                                                                                                                                                                                    KGFFRRSIQKNMVYTCHRDKNCIINKVTRNPCQYCRLQKCFEVGMSKESVRNDRNKKKKE 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                         SELSTKCIIKTVEFAKQLPGFTTLTIADQITLLKAACLDILILRICTRYTPEQDTMTFSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DMLQEPLLEALKVYVRKRRPSRPHMFPKMLMKITDLRSISAKGAERVITLKMEIPGSMPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chromosome mapping; gene mapping; gene therapy; forensic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
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                                                                                                                                                                                                                                                       Length 416;
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                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                     Score 2114; DB 20;
Pred. No. 4e-173;
2; Mismatches 2;
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Disclosure; Fig 3J-R; 447pp; English.
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                                                                                                                                                                                                                                                    86.78;
97.18;
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                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 402; Conserv
                                                                                                                                                                                                                           416 AA;
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                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                     Query Match
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polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG30010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YTPEQDTMTFSDGLTLNRTQMHNAGFGPLTDLVFAFANQLLPLEMDDAETGLLSAICLIC 331
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                                                                                                                                                                                                                                                                                    new isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TP---LRTPLWNGSNH-----SIETQSSSSEEIVPSPPSPPLPRIYKPCFVCQDKSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 2114; DB 22;
Pred. No. 5.8e-173;
2; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 20; SEQ ID No 49217; 103pp; English.
                                                                                                                                      Tang YT;
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Best Local Similarity 95.3%;
Matches 406; Conservative
                                                                                                                                                                                                      WPI; 2001-639362/73
                                                                                                                                      Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          547 AA;
                                                                   (HYSE-) HYSEQ INC.
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                                                                                       VEFAKQLPGFTTLTIADQITLLKAACLDILILRICTRYTPEQDTMTFSDGLTLNRTQMHN
                                                                                                                                                                                                                                                                                                                                                               LTPEVGELIEKVRKAHQETFPALCQLGKYTTNNSSEQRVSLDIDLWDKFSELSTKCIIKT
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Note: The sequence data for this patent did not appear in the printed product in the printed or the condition of the condition 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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ilarity 99.3%; Pred. No. 9e-173;
Conservative 1; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human diagnostic protein #20939.
                                                                                                                                                                                                         ABG20948 standard; Protein; 563 AA.
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542 PATHSP 547
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                             Human; chromosome mapping; gene mapping; gene therapy; forensic. food supplement; medical imaging; diagnostic; genetic disorder.
521 LDTLSGQPGGGGRDGGCLAPPGSCSPSLSPSSNRSSPATHSP 563
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                                                                                                                                                                                                            Novel human diagnostic protein #18853.
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                                                                                                      ABG18862 standard; Protein; 668
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23-AUG-2000; 2000US-0649167
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Local Similarity

Best Local Sim Matches 400;

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SIETQSSSSEELVPSPPSPPPLPRIYKPCFVCQDKSSGYHYGVSACEGCKGFFRRSIQKN 114

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05-FEB-1999
                                 Warrell RP
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a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and diagnostic amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                   MYYTCHRDKNCIINKVTRNPCQYCRLQKCFEVGMSKESVRNDRNKKKKEVPKPECSESYT 174
                                                                                                                                                                                                                                    234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Retinoic acid receptor; RAR-alpha; myl; acute promyelocytic leukemia; APL; translocation; chromosome 17; chromosome 15; PCR; primer; [t(15;17)(q21;q11-22)]; breakpoint; polymerase chain reaction.
                                                                                                                                                                                                                                                                                                                                                                                 KVYVRKRRPSRPHMFPKMLMKITDLRSISAKGAERVITLKMEIPGSMPPLIQEMLENSEG 414
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                                                                                                                                                 Length 668;
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                                                                                                                                              Score 2112; DB 22;
Pred. No. 1.1e-172;
1; Mismatches 2;
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91US-0675084
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                                                                                                                                                       Sest Local Similarity 99.3
Matches 400; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  myl/RAR-alpha fusion.
                                                                                                                             668 AA;
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22-MAR-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                        The sequence given shows a fusion between retinoic acid receptor (RAR)-alpha and myl which is characteristic of acute promyelocytic leukemia (APL). This is caused by a translocation of a portion of the long arm of chromosome 17 onto the long arm of chromosome 15 [t(15;17)(q21;q11-22)]. The breakpoint region has been cloned and has been shown that DNA rearrangements are clustered in the region of the first intron of RAR-alpha. This sequence was isolated by polymerase chain reaction (PCR) using primers which correspond to sequences both 5' and 3' to the breakpoint region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIETQSSSSEEIVPSPPSPPPLPRIYKPCFVCQDKSSGYHYGVSACEGCKGFFRRSIQKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MVYTCHRDKNCIINKVTRNPCQYCRLQKCFEVGMSKESVRNDRNKKKKEVPKPECSESYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             295 AGFGPLTDLVFAFANQLLPLEMDDAETGLLSAICLICGDRQDLEQPDRVDMLQEPLLEAL
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                                                                                                                                                                                                                  Marker for acute promyelocytic leukaemia and other neoplasias comprising nucleic acid and encoded abnormal retinoic acid
                                                      Miller WH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 797;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                        Kazizuka A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 2112; DB 13;
Pred. No. 1.5e-172;
L; Mismatches 2;
                                                      Evans RM, Frankel S,
(SLOK ) SLOAN KETTERING INST CANCER
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                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 4; 84pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86.7%;
ilarity 99.3%;
Conservative
                                                                                                                                                                                                                                                                           receptor-alpha receptor
                                                                                                                                        WPI; 1992-349240/42.
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Matches 400; Conserv
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                                                                                                                                                                  N-PSDB; AAQ29334
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                                                        Dmitrovsky E,
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Homo sapiens

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This sequence represents a human myl/RAR-alpha (retinoic acid receptor alpha) fusion protein which is used in a method for identifying a subject with acute promyelocytic leukaemia (APL) resulting from a t(15:17) translocation who will respond to treatment with all-trans retinoic acid. The protein can also be used to identify a subject with indications of APL who will not respond to treatment with all-trans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55 SIETQSSSSEEIVPSPPSPPLPRIYKPCFVCQDKSSGYHYGVSACEGCKGFFRRSIQKN 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MVYTCHRDKNCIINKVTRNPCQYCRLQKCFEVGMSKESVRNDRNKKKKEVPKPECSESYT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LTPEVGELIEKVRKAHQETFPALCQLGKYTTNNSSEQRVSLDIDLWDKFSELSTKCIIKT 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGFGPLTDLVFAFANQLLPLEMDDAETGLLSAICLICGDRQDLEQPDRVDMLQEPLLEAL 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Diagnosis of acute promyelocytic leukaemia - by detecting nucleic acid encoding abnormal retinoic acid receptor-alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KVYVRKRRPSRPHMFPKMLMKITDLRSISAKGAERVITLKMEIPGSMPPLIQEMLENSEG
                                                                                                                                                                                                                                                                                                                                                                                                                                86.7%; Score 2112; DB 20; Length 797; 99.3%; Pred. No. 1.5e-172; 1.ve 1; Mismatches 2; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            415 LDTLSGQPGGGRDGGGLPPPGSCSPSLSPSSNRSSPATHSP 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Warrell RP;
                                                                                                                                                              (SLOK ) SLOAN KETTERING INST CANCER RES.
                                                                                                                                                                                     Dmitrovsky E, Frankel S, Miller WH,
                                                                                                                                                                                                                                                                                   Disclosure; Fig 4A-G; 38pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABG18860 standard; Protein; 819
                                                                                                           93US-0095728.
91US-0673838.
91US-0675084.
                                                                                     93US-0095728
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 400; Conservative
                                                                                                                                                                                                            WPI; 1999-044563/04.
N-PSDB; AAV64990.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                          797 AA;
                                                                                                         21-JUL-1993;
22-MAR-1991;
22-MAR-1991;
                                                                                                                                                                                                                                                                                                                                                                                   retinoic acid
                                                                                    21-JUL-1993;
                                    US5843642-A
                                                           01-DEC-1998
              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, complete the reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as to foologinal expression or supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed setting in the content of the content of the content of intectly from WIPO at the content of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115 MYTCHRDKNCIINKVTRNPCQYCRLQKCFEVGMSKESVRNDRNKKKKEVPKPECSESYT 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                       gene therapy; forensic; stic; genetic disorder.
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Pred. No. 1.5e-172;
1; Mismatches 2;
                                                                                                                       n; chromosome mapping; gene mapping; gene
supplement; medical imaging; diagnostic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 20; SEQ ID No 49219; 103pp; English
                                                                     Novel human diagnostic protein #18851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86.7%;
99.3%;
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23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                        30-MAR-2001; 2001WO-US08631
                   18-FEB-2002 (first entry)
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Best Local Similarity 99.3:
Matches 400; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-639362/73.
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                                                                                                                                                                                             Homo sapiens
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                                                     414
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/label- Region C
/note- "DNA binding domain. 95 per cent amino acid
identity between mRAR's"
VEFAKQLPGFTTLTIADQITLLKAACLDILILRICTRYTPEQDTMTFSDGLTLNRTQMHN
      AGFGPLTDIVFAFANQLLPLEMDDAETGLLSAICLICGDRQDLEQPDRVDMLQEPLLEAL
                                 KVYVRKRRPSRPHMFPKMLMKITDLRSISAKGAERVITLKMEIPGSMPPLIQEMLENSEG
                                                                                                                                                                                                                              differential trans-activa-
                                                                                                                                                                                                                                                                                                                                                                                                                                                               . human and mouse retinoic acid receptors - encode proteins to assay for agonists and antagonists % \left( \frac{1}{2}\right) =0
                                                                                                                                                                                                                                                                                                                                                                                                                                  Ä;
                                                                                                                                                                               mouse; retinoic acid receptor; mRAR-alpha; embryogenesis
                                                                                                                                                                  Murine Retinoic Acid Receptor-alpha (deduced from cDNA).
                                                                                                                                                                                                                                    nuclear receptors"
                                                                                                                                                                                                                                                                                                                                                                                                                                  Zelent
                                                                                                                                                                                                                                       60..87
/label= Region B
^note= "well conserved between mRAR's"
                                                                                    LDTLSGQPGGGGRDGGGLPPPGSCSPSLSPSSNRSSPATHSP 457
                                                                                                                                                                                                                                                                                                                                                                                                                                 Petkovich M,
                                                                                                                                                                                                                                                                                                                         domain"
                                                                                                                                                                                                                                                                                             /label= Region D
/note= "putative hinge region"
                                                                                                                                                                                                                                                                                                                /label= Region E
/note= "ligand binding
                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                          AAR10547 standard; protein; 462 AA
                                                                                                                                                                                                                                                                                                                                                                                                                               Krust A,
Staub A;
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/label- Region F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 1; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                            (INRM ) INSERM INST NAT SANTE. (SQUI ) LES LABS SQUIBB SA.
                                                                                                                                                                                                                                                                                                                                                                                         90US-0502140.
89US-0374690.
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                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                 , Kastner
Mendelsoh
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                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                                                                                            29-JUN-1990;
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                                                                                                                                                    11-APR-1991
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An 11.5 day-old total mouse embryo lambda gtl0 cDNA library was screened with labelled human RAR-alpha probes. Positive clones were isolated, mapped and sequenced. A set of mRAR-alpha clones was identified on the basis of a 98 percent homology of their cDNA-deduced amino acid sequence with that of human RAR-alpha. There are 8 amino acid substitutions (mostly conservative) between the human and mouse sequences. See also AARIO548, AAQI0388-9 and AAQI0405-8.
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                                                                                                                                                                                                                                                                                              32 LGGLSP-PGALTSLQHQ------LPVSG-YSTP-----SPATIETQSSSSEEI
                                                                                                                                                                                                                                                                                                                                                    67 VPSPPSPPPLPRIYKPCFVCQDKSSGYHYGVSACEGCKGFFRRSIQKNMVYTCHRDKNCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                          LTIADQITLLKAACLDILILRICTRYTPEQDTMTFSDGLTLNRTQMHNAGFGPLTDLVFA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HMFPKMLMKITDLRSISAKGAERVITLKMEIPGSMPPLIQEMLENSEGLDTLSGQPGGGG
                                                                                                                                                                                                                                     20;
                                                                                                                                                                                            Length 462;
                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                            Score 2089; DB 12;
Pred. No. 6.5e-171;
8; Mismatches 17;
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/note= "C region"
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                                                                                                                                                                                            85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                 Matches 406; Conservative
                                                                                                                                                                                                            Local Similarity
                                                                                                                                                     462 AA;
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Sequence
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To proteins of mouse. This sequence represents the RAR-alpha sequence. The murine RAR-gamma sequence was used in the isolation of human RAR-gamma.

To murine RAR-gamma sequence was used in the isolation of human RAR-gamma.

RAR-gamma is a retinoic acid inducible transcription factor, and issues specifically in the skin where it is the predominant RAR. The control of the protein are the most highly conserved regions of the protein are the most highly conserved regions.

To and the E region is the ligand binding domain. The B region is also and the E region is the ligand binding domain. The B region is also conserved within species. The N and C terminal regions of segment D region is thought to act as a hinge region. Regions A and F remot conserved within a given species. The A, B, D and F regions are conserved across species, suggesting that they have specific functions, but are not required for the RAR's specific phylaological roles. The protein is used to detect competitive and non-competitive agonists and receptor expression in normal and diseased tissues and cultures.
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                                                                                                                                                                                                                                                         New cDNA encoding the human retinoic acid receptor gamma - useful for identifying agonists and antagonists of RAR-gamma and detecting expression in normal and diseased tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 VGGPTPNPFLVVDFYNQNRACLLPEKGLPAPGPYSTPLRTPLWNGSNHSIETQSSSSEEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RKAHQETFPALCQLGKYTTNNSSEQRVSLDIDLWDKFSELSTKCIIKTVEFAKQLPGFTT
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                                                                                                                                                                                                     Leroy P, Mendelsohn C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 16;
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90.0%; Pred. No. 6.5e-171
.1ve 8; Mismatches 17
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(BRIM ) INST RECH SQUIBB.
(BRIM ) LES LAB SQUIBB SA.
          420..462
/note= "F region"
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Zelent A;
  /note≈ "E region"
                                                                                                                                                                                                                                                                                                       Example 1; Fig 1; 34pp; English.
                                                                                              90EP-0110924.
                                                                                                                    90US-0502140
                                                                                                                               89US-0374690
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Matches 406; Conservative
                                                                                                                                                                                                   Kastner P,
                                                                                                                                                                                                              Stauba,
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                                                                                           29-JUN-1990;
                                                                                                                               30-JUN-1989;
                                                                                                                 29-MAR-1990;
                                             EP683227-A1
                                                                    22-NOV-1995
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in compactics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and canno acid sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
431
                                                                                                                                      HMFPKMLMKITDLRSISAKGAERVITLKMEIPGSMPPLIQEMLENSEGLDTLSGQPGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; chromosome mapping; gene mapping; gene therapy; forensi
food supplement; medical imaging; diagnostic; genetic disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                   RDGGGLPPPPGSCSPSLSPSSNRSSPATHSP 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel human diagnostic protein #18852.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-MAR-2000; 2000US-0540217, 23-AUG-2000; 2000US-0649167,
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470 AA;

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7;
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                                                                                                                                                                                                                                                                                             FAFANQLLPLEMDDA-ETGLLSAICLICGDRQDLEQPDRVDMLQEPLLEALKVYVRKRRP 363
                                                                                                                                                                                                                                                                                                                                                         TLTIADQITLLKAACLDILILRICTRYTPEQDTMTFS-DGLTLNRTQMHNAGFGPLTDLV 304
                                                                                                                                                                                                                                                                                                                                             SRPHMFPKMLMKITDLRSISAKGAERVITLKMEIPGSMPPLIQEMLENSEGLDTLSGQPG 423
                                                              37 LGGLSP-PGALTTLQHQ------SPATIETQSSSSEEI 76
                        23; Gaps
                                                7 VGGPTPNPFLVVDFYNQNRACLLPEKGLPAPGPYSTPLRTPLWNGSNHSIETQSSSSEEI 66
Query Match 83.2%; Score 2026.5; DB 22; Length 470; Best Local Similarity 88.5%; Pred. No. 1.6e-165; Matches 402; Conservative 7; Mismatches 22; Indels 23;
                                                                                                                                                                                                                                                                                                                                                                                                         437 GGGRDGGGLAPPPGSCSPSLSPSSNRSSPATHSP 470
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Search completed: March 29, 2003, 06:38:55 Job time : 58 secs

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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

US-09-691-220-2 2437 1 MYESVEVGGPTPNPFLVVDFSCSPSLSPSSNRSSPATHSP 457

Perfect score: Sequence:

Scoring table:

237916 seqs, 58723674 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

1. (1972-6. Prodata/1/Pubpaa/US08_NEW_PUB.pep:*
2. (1972-6. Prodata/1/Pubpaa/PCT_NEW_PUB.pep:*
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3. (1972-6. Prodata/1/Pubpaa/US08_PUBCOMB.pep:*
4. (1972-6. Prodata/1/Pubpaa/US08_PUBCOMB.pep:* Published_Applications_AA:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ				
Result		Query				
No.	Score	Match	Match Length DB	BB :	£	Description
-	2127	87.3	462	10	US-09-797-727-3	Seguence 3. Appli
7	2124	87.2	462	φ	US-09-814-604-1	Segmence 1. Appli
m	1771	72.7	448	σ	US-09-814-604-2	
4	1765	72.4	448	10	US-09-797-727-4	:
Ŋ	1662	68.2	454	6	US-09-814-604-3	``
φ	1662	68.2	454	10	US-09-797-727-2	Sequence 2. Appli
7	260	23.0	461	12	US-10-013-823-3	im
80	549	22.5	446	10	US-09-909-446-2	Sequence 2, Appli
σ	549	22.5	446	10	US-09-909-325-2	
10	549	22.5	446	10	US-09-909-326-2	
11	545	22.4	446	17	US-10-013-823-2	Sequence 2, Appli
12	519.5	21.3	598	10	US-09-853-386-32	32.
13	519.5	21.3	598	10	US-09-853-386-35	Sequence 35, Appl
14	519.5	21.3	598	10	US-09-853-386-36	36,
15	519.5	21.3	598	10	US-09-853-386-37	37,
16	519.5	21.3	598	10	US-09-853-386-38	38
17	519.5	21.3	298	10	US-09-853-386-39	39
18	519.5	21.3	598	10	US-09-853-386-40	40,
19	519.5	21.3	238	10	US-09-853-386-41	Sequence 41, Appl

Sequence 45, Appl Sequence 63, Appl Sequence 61, Appl Sequence 61, Appl Sequence 66, Appl Sequence 68, Appl Sequence 73, Appl Sequence 71, Appl Sequence 31, Appl Sequence 67, Appl Sequence 66, Appl Sequence 67, Appl Sequence 67, Appl Sequence 67, Appl Sequence 64, Appl	
US-09-853-386-45 US-09-965-703-63 US-09-965-703-63 US-09-965-703-61 US-09-965-703-61 US-09-853-386-66 US-09-853-386-66 US-09-853-386-73 US-09-853-386-73 US-09-952-559-3 US-09-952-559-3 US-09-953-386-91 US-09-853-386-91 US-09-853-386-91 US-09-853-386-91 US-09-853-386-91 US-09-853-386-96 US-09-853-386-96 US-09-853-386-67 US-09-853-386-65 US-09-853-386-65 US-09-853-386-65 US-09-853-386-66 US-09-853-386-66 US-09-853-386-66 US-09-853-386-66 US-09-853-386-66 US-09-853-386-66 US-09-853-386-66 US-09-853-386-66	
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ALIGNMENTS

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32 LGGLSP-PGALTILQHQ-------LPVSG-YSTP------SPATIETQSSSSEEI 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 VGGPTPNPFLVVDFYNQNRACLLPEKGLPAPGPYSTPLRTPLWNGSNHSIETQSSSSEEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature; OTHER INFORMATION: Human Retinoic Acid Receptor-alpha (hRAR-alpha): US-09-797-727-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 462;
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               Sequence 3, Application US/09797727

Patent No. US20020077457A1

SEGNERAL INROMATION:
APPLICANT: THE SAIK INStitute for Biological Studies
APPLICANT: TAKAKU, Fumimaro
TITLE OF INVENTION: GAMBA RETINOIC ACID RECEPTOR
FILE REPERENCE: SALKILI50-3
CURRENT APPLICATION NUMBER: US/09/797,727
CURRENT FILING DATE: 1201-08-31
PRIOR APPLICATION NUMBER: US 08/100,039
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: PCT/US90/03564
PRIOR APPLICATION NUMBER: PCT/US90/03564
PRIOR APPLICATION NUMBER: PCT/US90/03564
PRIOR PLILING DATE: 1990-06-22
PRIOR FILING DATE: 1990-06-22
NUMBER OF SEQ ID NOS: 7
SOSTWARE: PATENTING VERSION 3:0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 87.3%; Score 2127; DB 10;
Best Local Similarity 91.6%; Pred. No. 7.7e-166;
Matches 413; Conservative 5; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Human
US-09-797-727-3
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56 TQSTSSEELVPSPPSPLPPPRVXKPCFVCQDKSSGYHYGVSACEGCKGFFRRSIQKNMIY 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58 TQSSSSEEIVPSPPSPPPLPRIYKPCFVCQDKSSGYHYGVSACEGCKGFFRRSIQKNMVY 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MYESVEVGGPTPNPFLVVDFYNQN-RACLLPEKGLPAPGPYSTPLRTPLWNGSN--HSIE 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           356 IRKRRPSKPHWFPKILMKITDLRSISAKGAERVITLKMEIPGSMPPLIQEMMENSEGHEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                358 VRKRRPSRPHMFPKMLMKITDLRSISAKGAERVITLKMEIPGSMPPLIQEMLENSEGLDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                238 AKQLPGFTTLTIADQITLLKAACLDILILRICTRYTPEQDTMTFSDGLTLNRTQMHNAGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 178 EVGELIEKVRKAHQETFPALCQLGKYTTNNSSEQRVSLDIDLWDKFSELSTKCIIKTVEF
                                                                                                                                                                   Sequence 2, Application US/08814604

Publication No. US20030003517A1

GENERAL INFORMATION:

APPLICANT: Klein, Elliott S.

APPLICANT: Chandraratha Roshantha A.

TITLE OF INVENTION: Methods of Detecting Dissociated Nuclear

TITLE OF INVENTION: Methods of Detecting Dissociated Nuclear

FILE REPERENCE: P-AK 4528

CURRENT APPLICATION NUMBER: US/09/814,604

CURRENT PILING DATE: 2001-03-22

NUMBER OF SEQ ID NOS: 52

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 448;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: The Salk Institute for Biological Studies APPLICANT: TAKAKU, Fumimaro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  418 LSGQPGGGGRDGGGLPPPPGSCSPSLSPSSNRSSPATHSP 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72.7%; Score 1771; DB 9; 74.3%; Pred. No. 9.1e-137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42; Mismatches
                                                                               RDGGGLPPPPGSCSPSLSPSSNRSSPATHSP
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US-09-797-727-4
Sequence 4, Application US/09797727
Patent No. US20020077457A1
GENERAL INFORMATION:
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Matches 342; Conservative
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US-09-814-604-2
                                                                                                                                             RESULT 3
US-09-814-604-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127 INKVTRNPCQYCRLQKCFEVGMSKESVRNDRNKKKKEVPKPECSESYTLTPEVGELIEKV 186
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                                                                               LTIADQITLLKAACLDILILRICTRYTPEQDTMTFSDGLTLNRTQMHNAGFGPLTDLVFA 306
                                                                                                                                                                                            FANQLLPLEMDDAETGLLSAICLICGDRQDLEQPDRVDMLQEPLLEALKVYVRKRRPSRP 366
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                  Gaps
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                                                                                                                                                RKAHOETFPALCOLGKYTTNNSSEORVSLDIDLWDKFSELSTKCIIKTVEFAKOLPGFTT
                                                                                                                                                                                                           32 LGGLSP-PGALTTLQHQ------LPVSG-YSTP-----SPATIETQSSSSEEI
                                                                RKAHQETFPALCQLGKYTTNNSSEQRVSLDIDLWDKFSELSTKCIIKTVEFAKQLPGFTT
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Pred. No. 1.4e-165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Chandraratna Roshantha A.
APPLICANT: Chandraratna Roshantha A.
TITLE OF INVENTION: Methods of Detecting Dissoci:
TITLE OF INVENTION: Hormone Receptor Ligands
FILE REFERENCE: P-AR 4528
CURRENT APPLICATION NUMBER: US/09/814,604
CURRENT FILING DATE: 2001-03-22
NUMBER OF SEQ ID NOS: 52
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Mismatches
                                                                                                                                                                                                                                                                                                                                      RDGGGLAPPPGSCSPSLSPSSNRSSPATHSP 462
                                                                                                                                                                                                                                                                                                                           RDGGGLPPPPGSCSPSLSPSSNRSSPATHSP 457
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Best Local Similarity 91.4%;
Matches 412; Conservative
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SOFTWARE: FastSEQ for Windows Version 4.0
                                       TYPE: PRT
CORGANISM: Homo sapiens
US-09-814-604-3
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US-09-797-727-2
                            LENGTH: 454
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               SEQ ID NO 3
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                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
OTHER INFORMATION: Human Retinoic Acid Receptor-beta (hRAR-beta)
                                                                                                                                                                                                                                                                                                                  Length 448;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Klein, Elliott S.
APPLICANT: Chandraratna Roshantha A.
TITLE OF INVENTION: Methods of Detecting Dissociated Nuclear
TITLE OF INVENTION: Hormone Receptor Ligands
FILE REFERENCE: P-AR 4528
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Best Local Similarity 74.1%; Pred. No. 2.8e-136;
Matches 341; Conservative 43; Mismatches 58;
 OF INVENTION: GAMMA RETINOIC ACID RECEPTOR
         FILE REFERENCE: SALK1150-3
CURRENT APPLICATION NUMBER: US/09/797,727
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: US 08/100,039
PRIOR FILING DATE: 1995-06-07
PRIOR PELICATION NUMBER: US 08/100,039
PRIOR FILING DATE: 1993-07-30
PRIOR FILING DATE: 1990-06-22
PRIOR FILING DATE: 1990-06-22
PRIOR FILING DATE: 1990-06-22
PRIOR PELICATION NUMBER: US 07/370,407
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CURRENT FILING DATE: 2001-03-22
NUMBER OF SEQ ID NOS: 52
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                                                                                                                                                              NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                 ORGANISM: Human
                                                                                                                                                                                                       LENGTH: 448
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                                                                                                                                                                                          SEQ ID NO 4
                                                                                                                                                                                                                     TYPE: PRT
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NQLLPLEMDDAETGLLSAICLICGDRQDLEQPDRVDMLQEPLLEALKVYVRKRRPSRPHM 368
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                                                                                                                                  16 PGSGYPGAGFPFAFPGALRGSPPFEMLSPSFRGLGQPDLPKEMASLSVETQSTSSEEMVP 75
                                                                                                          ---SNHSIETQSSSSEEIVP 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; NAME/KEY: misc_feature
; OTHER INFORMATION: Human Retinoic Acid Receptor-gamma (hRAR-gamma)
US-09-797-727-2
                                                       32;
Length 454;
                                                     Indels
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Sequence 2. Gapplication US/0979727

Patent No. US/20020077457A1

GENERAL INFORMATION:

APPLICANT: The Salk Institute for Biological Studies APPLICANT: The Salk Institute for Biological Studies APPLICANT: TARKU, Funnaro

TITLE OF INVENTION: GAMMA RETINOIC ACID RECEPTOR FILE REFERENCE: SALK1150-3

CURRENT APPLICATION NUMBER: US/09/797,727

CURRENT FILING DATE: 2001-08-31

PRIOR FILING DATE: 1995-06-07

PRIOR APPLICATION NUMBER: US 08/100,039

PRIOR APPLICATION NUMBER: PCT/US90/03564

PRIOR FILING DATE: 1990-06-22

PRIOR FILING DATE: 1990-06-22

PRIOR FILING DATE: 1990-06-22

PRIOR FILING DATE: 1990-06-22

NUMBER OF SEQ ID NOS: 7

SOFTWARE: Patentin Version 3.0
  ; Score 1662; DB 9;
; Pred. No. 7.5e-128;
39; Mismatches 48;
                                                                                                       30 PEKGLPAPG-PYSTP-----LRTPLWNG----
     68.2%;
72.8%;
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  Query Match
Best Local Similarity 72.8
Matches 319; Conservative
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----PLPRI--YKPCFVCQDKSSGYHYGVSACEGCKGFFRRSIQKNMV--YTCHRDKNCI 126
                                                                                                                                                                193 SSASGPGASPGGSEAGSQGSGEGEGVQLTAAQELMIQQLVAAQLQCNKRSFSDQPKVTPW 252
                                                                                                                                                                                                                    253 PLGADPQSRDARQORFA-----HFTELAIISVQEIVDFAKQVPGFLQLGREDQIALLK 305
                                                                                                                                                                                                                                                                AACLDILILRICTRYTPEQDTMTFSDGLTLNRTQMHNAGFG-PLTDLVFAFANQLLPLEM 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GUSTAFSSON, JAN
TITLE OF INVENTION: OR-1 ON ORPHAN RECEPTOR BELONGING
TO THE NUCLEAR RECEPTOR FAMILY
                                                                  INKVTRNPCQYCRLQKCFEVGMSKESVRNDRNKKKKEVPKPECSESYTLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.C
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/909,446
FILING DATE: 19-0ul-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                 377 TDLRSISAKGAERVITLKMEIPGSMPPLIQEMLENSE 413
                                                                                                                                                                                                                                                                                                                                                                                                                                  426 VSLRTLSSVHSEQVFALRLQ-DKKLPPLLSEIWDVHE 461
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REGISTRATION NUMBER: 32141
REFERENCE/DOCKET NUMBER: 00487.04029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/776,844
FILING DATE: <UNKNOWN>
APPLICATION NUMBER: UK 9413536.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff
STREET: 1001 G Street, NW
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 16-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09909446 Patent No. US20020052489A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 202-508-9100
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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                                                                         30 PEKGLPAPG-PYSTP------LRTPLWNG-----SNHSIETQSSSEEIVP
                                                                                                                                                                                                                                                                          189 AHQETFPALCQLGKYTTNNSSEQRVSLDIDLWDKFSELSTKCIIKTVEFAKQLPGFTTLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FPKMLMKITDLRSISAKGAERVITLKMEIPGSMPPLIQEMLENSEGLDTLSGQPG----
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Patent No. US20020116731A1
GENERAL INFORMATION:
APPLICANT: Guenther, Catherine
APPLICANT: Allen, Keith D.
APPLICANT: Allen, Keith D.
APPLICANT: Baribault, Helene
TITLE OF INVENTION: TRANSGENIC MICE CONTAINING RETINOID X
TITLE OF INVENTION: RECEPTOR INTERACTING FROTEIN GENE DISRUPTIONS
                                               32;
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          Length 454;
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                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                               48;
            Score 1662; DB 10;
Pred. No. 7.5e-128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; DB 12;
8.8e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches 155;
68 2%; st. 72.8%; Pred. No. ... 39; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: R-684
CURRENT APPLICATION NUMBER: US/10/013,823
CURRENT FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: US 60/254,801
PRIOR PELING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: US 60/309,404
PRIOR FILING DATE: 2001-07-31
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23.0%; Score 560; 30.6%; Pred. No. 8
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        Query Match
Best Local Similarity 72.89
Matches 319; Conservative
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Best Local Simmatches 140;
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US-10-013-823-3
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76 LPRI--YKPCFVCQDKSSGYHYGVSACEGCKGFFRRSIQKNMV--YTCHRDKNCIINKVT 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                189 TSEASSQGSGEGEGIQLTAAQELMIQQLVAAQLQCNKRSFSDQPKVTPWPLGADPQSRDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     269 CTRYTPEQDTMTFSDGLTLNRTQMHNAGFG-PLTDLVFAFANQLLPLEMDDAETGLLSAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                328 CLICGDRQDLEQPDRVDMLQEPLLEALKVYVRKRRPSRPHMFPKMLMKITDLRSISAKGA
                                                                                                                                                                                                                                                                                                                                             Length 446;
                                                                                                                                                                                                                                                                                                                                                                                                                      29 LPEKGLPAPGPYSTPLRTPLWNGSNHSIE----TQSSSSEEIVP--SPPSPP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GUSTAFSSON, JAN
TITLE OF INVENTION: OR-1 ON ORPHAN RECEPTOR BELONGING
TO THE NUCLEAR RECEPTOR FAMILY
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                         22.5%; Score 549; DB 10; 31.6%; Pred. No. 6.7e-37; Live 75; Mismatches 158;
               NAME: Kagan, Sarah A
REGISTARION UNBER: 32141
REFERENCE/DOCKET NUMBER: 00487.04029
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     169 CSESYTLTPEVGELIEKVRKAH---QETFPALCQLGKYT-
                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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ADDRESSEE: Banner & Witcoff
STREET: 1001 G Street, NW
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                                                                                          TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 446 amino acids
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Patent No. US20020128461A1
GENERAL INFORMATION:
APPLICANT: ENMARK, EVA
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                           STRANDEDNESS: single
                                                                                                                              TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 2:
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                                                                                                                                                                                                         TYPE: amino acid
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US-09-909-326-2
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                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                12;
                                                                                                                                                                                                                                                                189 TSEASSQGSGEGEGIQLTAAQELMIQQLVAAQLQCNKRSFSDQPKVTPWPLGADPQSRDA 248
                                                                                                                                                                                                                                                                                                                                         CSESYTLTPEVGELIEKVRKAH---QETFPALCQLGKYT------TINNS 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        209 SEQRVSLDIDLWDKFSELSTKCIIKTVEFAKQLPGFTTLTIADQITLLKAACLDILILRI 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301
                                                                                                                                                                                                                                          76 LPRI--YKPCFVCQDKSSGYHYGVSACEGCKGFFRRSIQKNMV--YTCHRDKNCIINKVT 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   269 CTRYTPEQDIWIFSDGLTLNRTQMHNAGFG-PLTDLVFAFANQLLPLEMDDAETGLLSAI 327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLICGDRQDLEQPDRVDMLQEPLLEALKVYVRKRRPSRPHMFPKMLMKITDLRSISAKGA 387
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                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72;
                                                                                            Length 446;
                                                                                                                                                               29 LPEKGLPAPGPYSTPLRTPLWNGSNHSIE----TQSSSSEEIVP--SPPSPP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: OR-1 ON ORPHAN RECEPTOR BELONGING TO THE NUCLEAR RECEPTOR FAMILY
                                                                                                                            158; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.0
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COMPUTER: IBM COMPALIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.
RRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/909,325
FILING DATE: 19-Jul-2001
CLASSIFICATION: <UNKNOWN>
                                                                                    ; Score 549; DB 10;
; Pred. No. 6.7e-37;
75; Mismatches 158;
                                                                                                                                                                                                                                                                                                                    132 RNPCQYCRLQKCFEVGMSKESVRNDRNKKKKEVPK-----
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APPLICATION NUMBER: UK 9413536.2
FILING DATE: 16-AUG-1994
         MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 08/776,844
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff
STREET: 1001 G Street, NW
CITY: Washington
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Patent No. US20020115847A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: ENMARK, EVA
GUSTAFSSON, JAN
                                                                                  Query Match 22.5%;
Best Local Similarity 31.6%;
Matches 141; Conservative 7
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                                               US-09-909-446-2
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Query Match
Best Local Similarity 31.4%
Matches 140; Conservative
                                Allen, Keith D.
Zhang, Qin
                                                                                                                                                                                                                                                                                                      ; ORGANISM: Mus musculus US-10-013-823-2
                                                                                                                                                                                                                                                                         446
                                APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                           TYPE: PRT
                                                                                                                                                                                                                                                        SEQ ID NO 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  189 TSEASSQGSGEGEIQLTAAQELMIQOLVAAQLQCNKRSFSDQPKVTPWPLGADPQSRDA 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                269 CTRYTPEQDIMTFSDGLTLNRTQMHNAGFG-PLTDLVFAFANQLLPLEMDDAETGLLSAI 327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29 LPEKGLPAPGPYSTPLRTPLWNGSNHSIE----TQSSSSEEIVP--SPPSPP-----P 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 LPGNGSPQPSTSST---SPIKEECQETDPPPGSECSSSAYIVVILEPEDEPERKRKKGP 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 446;
           COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 22.5%; Score 549; DB 10;
Best Local Similarity 31.6%; Pred. No. 6.7e-37;
Matches 141; Conservative 75; Mismatches 158;
                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 00487.04029
TELECOMMUTCATION:
TELEBHONE: 202-508-9100
TELEPRAX: 202-508-9299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CSESYTLTPEVGELIEKVRKAH---QETFPALCQLGKYT--
                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/776,844
FILING DATE: 1997-06-24
APPLICATION NUMBER: UK 9413536.2
FILING DATE: 16-AUG-1994
ATTORNEY,AGENT INFORMATION:
NAME: Kagan, Sarah A
REGISTRATION NUMBER: 32141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               132 RNPCQYCRLQKCFEVGMSKESVRNDRNKKKEVPK----
                                                                        APPLICATION NUMBER: US/09/909,326
FILING DATE: 19-Jul-2001
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-909-326-2
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EQVFALRLQ-DKKLPPLLSEIWDVHE 446
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Patent No. US20020116731A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 446 amino acids
MEDIUM TYPE: Diskette
                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
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US-10-013-823-2
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Suppression of the NURR
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TITLE OF INVENTION: TRANSGENIC MICE CONTAINING RETINOID X
TITLE OF INVENTION: RECEPTOR INTERACTING PROTEIN GENE DISRUPTIONS
FILE REFERENCE: R-684
CURRENT APPLICATION NUMBER: US/10/013,823
CURRENT FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: US 60/254,801
PRIOR PILING DATE: 2000-12-11
PRIOR PLILING DATE: 2000-12-11
PRIOR FILING DATE: 2001-07-31
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APPLICANT: Murphy, Evelyn
APPLICANT: Bresnihan, Barry
APPLICANT: Conneely, Orla
APPLICANT: Conneely, Orla
APPLICANT: Conneely, Orla
TITLE OF INVENTION: Therapeutic Approaches to Diseases by Suppre
TITLE OF INVENTION: Subfamily of Nuclear Transcription Factors
FILE REFERENCE: P01972US1
CURRENT APPLICATION NUMBER: US/09/853,386
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31.4%; Pred. No. 1.4e-36;
iive 75; Mismatches 159;
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                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
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422 EQVFALRLQ-DKKLPPLLSEIWDVHE 446
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Sequence 36, Application US/09853386
Patent No. US20020049151A1
GENERAL INFORMATION:
APPLICANT: Murphy, Evelyn
APPLICANT: Dresnihan, Barry
APPLICANT: Conneely, Orla
APPLICANT: Fitzgerald, Oliver
TITLE OF INVENTION: Therapeutic Approaches to Diseases by Suppression of the NURR
TITLE OF INVENTION: Subfamily of Nuclear Transcription Factors
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              Gaps
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                                                                             NRACLLPEKGLPAPGPYST-----PLRTPLWN----GSNHSIETQSSSSEEIVPSP-- 70
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              Indels
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          Mismatches 154;
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CURRENT APPLICATION NUMBER: US/09/853,386
CURRENT FILING DATE: 2001-05-11
PRIOR FILING DATE: 2000-05-12
PRIOR FILING DATE: 2000-05-12
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Best Local Similarity 31.5
Matches 141; Conservative
              Matches 141; Conservative
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CRGANISM: Mus musculus
US-09-853-386-36
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SEQ ID NO 36
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Patent No. US20020049151A1
GENERAL INFORMATION:

APPLICANT: Murphy, Evelyn
APPLICANT: Conneely, Orla
APPLICANT: Conneely, Orla
APPLICANT: Fitzgerald, Oliver
TITLE OF INVENTION: Therapeutic Approaches to Diseases by Suppression of the NURR
TITLE OF INVENTION: Subfamily of Nuclear Transcription Factors
CURRENT APPLICATION NUMBER: US/09/853,386
CURRENT FILING DATE: 2001-05-11
PRIOR PILING DATE: 2000-05-12
NUMBER OF SECIENCE: 2000-05-12
NUMBER OF SECIENCE: 2000-05-12
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       60/203645
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PRIOR APPLICATION NUMBER: US 6/
PRIOR FILING DATE: 2000-05-12
NUMBER OF SEQ ID NOS: 153
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 32
LENGTH: 598
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31.5%;
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US-09-853-386-35
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US-09-853-386-35
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LENGTH: 598
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Sequence 37, Application US/09853386

Patent No. US20020049151A1

GENERAL INFORMATION:

APPLICANT: Murphy, Evelyn

APPLICANT: Bresnihan, Barry

APPLICANT: Conneely, Orla

APPLICANT: Conneely, Orla

TITLE OF INVENTION: Therapeutic Approaches to Diseases by Suppression of the NURR

TITLE OF INVENTION: Therapeutic Approaches to Diseases by Suppression of the NURR

TITLE OF INVENTION: Therapeutic Approaches to Diseases by Suppression of the NURR

TITLE OF INVENTION: Subfamily of Nuclear Transcription Factors

CURRENT FILING DATE: 2001-05-11

PRIOR FILING DATE: 2000-05-12

NUMBER OF SEQ ID NOS: 153

SOFTWARE: PATENTI VERSION 3.1

SEQ ID NO 37

LENGTH: 598
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286 FFKRTVQKNAKYVCLANKNCPVDKRRRNRCQYCRPQKCLAVGMVKEVVRTDSLKGRRGRL 345
                                  165 P-KPECSESYTLTPEVGELIEKVRKAHQETFPALCQLG-----KYTTNNSSEQRVSL 215
                                                                                                      216 DIDLWDKFSELSTKCIIKTVEFAKQLPGFTTLTIADQITLLKAACLDILILRICTRYTPE 275
                                                                                                                               |::| ||: || :: || :| 517 GLKEPKRVEELQNKIVNCLKDHVTFNNGGLNRPNYLSKLLGKLPELRTLCTQGLQRIFYL 576
                                                      276 ODIWIFSDGLILNRIQMHNAGFGPLIDLVFAFANQLLPLEMDDAETGLLSAICLICGDRQ 335
                                                                                                                                                                                                                                                DLEQPDRVDMLQEPLLEALKVYVRKRRP--SRPHMFPKMLMKITDLRSISAKGAERVITL 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                106 FFRRSIOKNMVYTCHRDKNCIINKVTRNPCQYCRLOKCFEVGMSKESVRNDRNK-KKKEV 164
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; Pred. No. 2.6e-34;
79; Mismatches 154; Indels 73;
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31.5%;
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Best Local Similarity 31.54
Matches 141; Conservative
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; ORGANISM: HUMAN
US-09-853-386-37
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GenCore version 5.1.4_p5_4578

	Copyright (c) 1993 - 2003 Compugen Ltd.
OM nucleic - nu	OM nucleic - nucleic search, using sw model
Run on:	<pre>March 30, 2003, 08:00:38 ; Search time 2120.41 Seconds</pre>
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Sequence:	logo 1 gtccttgggtagcatgtacaacatgccgcctctccctctc 1000
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

TES	297538 · AJ297538 90426 AC090426					H																				AC127076 AC127076 Rattus							ALIGNMENTS	;	16913 bp DNA 11near PRI 06-JAN-2001 RARA gene, intron 2.		l receptor alpha.	Craniata; Vertebrata; E	Catarrhini
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us-09-691-220-3_copy_1_1000.rge

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AC090426 138999 bp DNA linear PRI 29-MAY-2002
Homo sapiens chromosome 17 clone 205m17 map 17q21.1, complete
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I bases 1 to 18999)
Gu,B., Xiong,H., Zhou,Y., Chen,B., Lu,L., Zhong,M., Yin,H., Huang,W., Ren,S., Chen,S.F., Chen,Z. and Fu,G.
Variant-type PML-RAR(alpha) fusion transcript in acute promyelocytic leukemia: use of a cryptic coding sequence from intron 2 of the RAR(alpha) gene and identification of a new clinical subtype resistant to retinoic acid therapy 22028997
12032336
                                                                                                             9981 GTCACACATGATGTCACAGACAATGACACAGCGGGTGTCTCATTCCGACACAGGGTCCG 10040
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       9861 GAGACACCTTGGGCGGGGCTTTGCTCGCCGGAAGCACGCAGAGCGTGGGGAGGAGGGCCC 9920
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                                Cross N.C.P., Department of Haematology, of Medicine, Hammersmith Hospital, London,
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Pred. No. 1.5e-188;
0; Mismatches 9;
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repeat_region 82688411 /rpt_family="Simple_repeat" /rpt_unit=(TGGG)n 92249532 /rpt_family="SINE/Alu" /rpt_unit=AluY repeat_region 95469639	/rpt_family="Low_complexity" /rpt_unit=cT-rich ropeat_region 1002510426 /rpt_family="LTR/Retroviral" /rpt_unit=MLT2A /rpt_unit=MLT2A /rpt_family="Simple_repeat" /rpt_unit=(TA)n /rpt_unit=(TA)n	/rpt_family="LTR/R" /rpt_unit=MLT2A complement(10675. /rpt_family="SINE/ /rpt_unit=AluY 11013. 11321 /rpt_family="SINE/ /rpt_family="SINE/ /rpt_family="SINE/ /rpt_family="SINE/	repeat_region complement(1184012192) /rpt_family="LTR/Mal.R" /rpt_unit=MGTD repeat_region 1272912835 /rpt_family="SINE/Alu" /rpt_unit=FLAM_A repeat_region /rpt_family="L1891) /rpt_family="LINE/L2"		repeat_region 1531115473 /rpt_family="Simple_repeat" /rpt_unit="[TA]n repeat_region 156915981 /rpt_family="SINE/Alu" /rpt_unit=AluSx repeat_region 163161633 /rpt_family="Simple_repeat" /rpt_family="Simple_repeat" /rpt_lamily="Simple_repeat" /rpt_family="Simple_repeat" /rpt_family="Simple_repeat" /rpt_family="Simple_repeat" /rpt_family="Simple_repeat"	repeat_region 17026: 17324 /rpt_tamily="SINE/Alu" /rpt_unit-Alusg /rpt_unit-Alusg /rpt_unit-Alusg /rpt_tamily="SINE/Alu" /rpt_unit-Alusx /rpt_unit-Alusx /rpt_unit-Alusx /rpt_unit-Alusx	/rpt_unit_frE54 repeat_region complement(1802618086) /rpt_unit=MIR" /rpt_unit=MIR" /rpt_unit=MIR" /rpt_dunit=MIR" /rpt_family="SINE/Alu" /rpt_family="SINE/Alu" /rpt_family="SINE/Alu" /rpt_family="SINE/Alu" /rpt_unit=AluSx repeat_region complement(1894819264) /rpt_unit=AluSx repeat_region complement(2001220168)
u, L., Zhong and Fu, G. onal Human P.R.China	PEATURES Center code: CHGC Website: http://www.chgc.sh.cn Contact: fugang@chgc.sh.cn. fugang@chgc.sh.cn. Location/Oualifiers source 1.138999 /db_xref="taxon:9606" /chromosome="17" /map="17421.1"	repeat_region 387.483 /rpt_finally="SINE/MIR" /rpt_unit=MIR repeat_region 725.1032 /rpt_family="SINE/Alu" /rpt_unit=AluJb repeat_region 1033.1198	repeat_region 1217.1514 "SINE/Alu" /rpt_family="SINE/Alu" /rpt_tamily="SINE/Alu" /rpt_unit=AluSp repeat_region complement(15341754) /rpt_family="SINE/MIR" /rpt_family="SINE/MIR" /rpt_family="SINE/MIR" /rpt_family="SINE/MIR" /rpt_family="SINE/MIR"	//pt_lamin_y sink_Mark //rpt_unit=Mirk //rpt_unit=Mirk complement(2607, 2665) //rpt_family="Sink_Mir" //rpt_family="Sink_Mir" //rpt_unit=Mirk //rpt_family="Link_Link" //rpt_family="Link_Link" //rpt_lamily="Link_Link_Link_Link_Link_Link_Link_Link_	repeat_region 40304213 /rpt_family="LTR/MalR" /rpt_family="LTR/MalR" /rpt_unit=MSTD /rpt_tamily="SINE/Alu" /rpt_tamily="SINE/Alu" /rpt_unit=AluJb /rpt_unit=AluJb /rpt_unit=AluSx repeat_region 45144811 /rpt_unit=AluSx	/rpt_unit_wsln" /rpt_unit_wsln /rpt_unit_wsln /rpt_inilly=LiNe/Lin /rpt_inilly=Line/Lin /rpt_inilly=Line/Lin /rpt_inilly=Line/Lin /rpt_family=Line/Rin /rpt_family=Rine/MIR* /rpt_inilly=Rine/Line/Line /rpt_inilly=Rine/MIR*	

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Anderson, S., Barna, N., Bastien, V., Beda, F., Boguslavkiy, L.,
Anderson, S., Barna, N., Bastien, V., Beda, F., Boguslavkiy, L.,
Boukhgalter, B., Brown, A., Burkett, G., Campoplano, A., Castle, A.,
Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,
Perreliano, K., Dewar, K., Data, J.S., Dodde, S., Ferreira, P.,
Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M.,
Graham, L., Grand-Pierre, N., Hagos, B., Haeford, A., Horton, L.,
Illev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., LaRocque, K.,
Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G.,
McChand, D., Marquis, N., McCarthy, M., McEwan, P., McKernan, K.,
McPheeters, R., Meldin, J., Meneus, L., Mihova, T., Mlanga, V.,
Morrow, J., Murphy, T., Naylor, J., Norman, C. H., O'Connor, T.,
O'Donnell, P., O'Meil, D., Ollyar, T. M., Ollver, J., Peterson, K.,
Pierre, N., Pisani, C., Pollara, V., Raymond, C., Rieback, M., Riley, R.,
Sougnez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Strauss, N., Subramainan, A., Talamas, J., Tesfaye, S., Theodore, J.,
Tirrell, A., Travers, M., Trigilio, J., Vassillev, H., Viel, R., Vo, A.,
Milson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J.,
Pierre, M., And Cody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo saplens chromosome 17 clone CTD-2267D19 map 17, *** SEQUENCING IN PROGRESS ***, 3 unordered pleces.
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Birren, B., Nusbaum, C. and Lander, E. Homo sapiens chamosome 17, clone CTD-2267D19
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                                                                                                                     GTCCTTGTCCCCTCGCAGCCCCCTCCTCTCCCTGTACTCGCCGTCCCTCTGTACTCTGTG 900
                                                    601 GGTCACTCGGAGGTGAGGCGCCGCCAGGCGAGTTCAGCGAGAGTTCAGCCGCATTGCATT
                                                                                                                                                                          AGGCAAATGAGGCCCGGCCTGGGTGGGGGTGTGTTAAGGGGAGGACACCGGGACCACC
                                                                                                                                                                                                                                           CCCCTCTTCCCCGCCCCACCTCCTCCACGGCTTCGCTCGGCCAGGGACTGACCA
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Pred. No. 1.2e-188;
0; Mismatches 9;
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complement(23861, 23963)
/rpt_family="LINE/LI"
/rpt_unit=LING4
complement(23975, 24084)
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         /rpt_unit=MIR
20326. 20637
/rpt_family="SINE/Alu"
/rpt_unit=AluSx
20955. 20992
/rpt_family="Simple_repeat"
/rpt_unit=(TTTA)n
                                                                                                                           complement(20993. .21282)
/rpt_family="SINE/Alu"
/rpt_unit=AllJO
21956. .50413
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complement(25845. .26039)
/rpt_family-"SINE/Alu"
/rpt_unit-AluSx
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25268. .25554
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                                                          Signates I. C. 1/344, Lander, E., Ali, A., Allen, N., Anderson, S., Barren, B., Nusbaum, C., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Coolymore, A., Cooke, P., DeArellano, K., Daray, J. S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C., Macarthy, M., Meldrim, J., Mender, M., Micol, R., Indonan, C., Norbu, C., Spencer, B., Stange-Thoman, N., Stojanovic, M., Talamas, J., Reige, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Zembek, L., Zimmer, A. and Zody, M., Wilson, B., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., Wiman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., Wiman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., Wiman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., Zembek, L., Zimmer, A., Wilson, B., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A., Wilson, B., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A., Wilson, B., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A., Wilson, B., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A., Wilson, B., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A., Wilson, B., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A., Wilson, B., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A., Wilson, B., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A., Wilson, B., Wyman, D., 
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Submitted (24-SEP-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 3 (bases 1 to 173441)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (14-AUG-2002) Whitehead Institute/AUT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 14, 2002 this sequence version replaced g1:22123315.

All repeats were identified using RepeatMasker:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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.2e-188;
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/clone_lib="CITD1 Human BAC"
4334 c 40918 g 42114 t
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Pred. No. 1.2
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Matches 990;
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AC131063 188574 bp DNA linear HTG 16-AUG-2002
Homo sapiens chromosome 17 clone RP11-1029L16 map 17, WORKING DRAFT
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                82544 TCCTTTTATCTCCAGAGCTGGACAGTGCACCAGGGGCCGGTACTGGTTCCCCAGCTAG 82485
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Submitted (16-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center: Whitehead Institute/ MIT Center for Genome Research
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contact: sequence_submissions@qenome.wi.mit.edu
center project Information
center clone name: L27554
center clone name: L27554
center clone name: 1029_L16
sequencing vector: plasmid; n/s; 100% of reads
Sequencing vector: plasmid; n/s; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
consensus quality: 187624 bases at least 030
consensus quality: 187650 bases at least 030
consensus quality: 187650 bases at least 020
Insert size: 187000: agarose-fp
Insert size: 188074; sum-of-contigs
Quality coverage: 14.6 in 020 bases; sum-of-contigs
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Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RW/RepeatMasker.html
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2173 19348: contig of 17176 bp in length
19349 19448: gap of 100 bp
19449 34798: contig of 15350 bp in length
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74761 151113: contig of 76353 bp in length
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                            Birren, B., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 17, clone RP11-1029L16
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/chromosome="17"
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DD 166326 GTCCTTGGGTAGCATGTACATTTCCATCCTTCTTTAGAGAGTGGGGGGTAATAGGATAC 166267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Db 166146 TCCTTTAACTCTCCCAGAGCTGGACACACGGGCCGGGAACTGGTACCTCCCAGCTAG 166087
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db 166086 GAGACCTTGGGCGGGCTTTGCTCGCCGGAAGCACGCAGAGCGTGGGGAGGAGGAGGAGCCC 166027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db 166026 CCTCTGCCTGTGTTTGTGCCAACAGCACCCGCGCTGCCGCGTCGGGTTCCGGCGCCGGA 165967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       165966 GTCACACATGATGTCACAGACAATGACACAAGCCGGTGTCTCATTCCGACACAGGGGTCCG 165907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DD 165666 TAGGCAAATGAGGCCCGGCCTGGGTGGGGGTGTGTTTTAAGGGGAGGACACCGGGACCAC 165607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       165727
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 CCCCTCCTCCAGGGGTATCCCCTCTTTCTAGGGACCTACCCAAGCTAGGCCTTTCTTCTA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 TCCTTTTATCTCTCCAGAGCTGGACAGTGCACCAGGGGCCGGTACTGGTTCCCCCAGCTAG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 GTGAAACGTGCATCCCGAGGGCTTCTAGGATGAAGTAGTCCACTGGAAGGCACCAGCTCT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 GAGACACCTTGGGCGGGCCTTTGCTCGCCGGAAGCACGCAGAGCGTGGGGAGGAGGAGGCCC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GTCCTTGGGTAGCATGTACATTTCCATCCCTTCCTTTTATATATGGGGGTAATAGGATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTCACACATGATGTCACAGACAATGACACAAGCCGGTGTCTCATTCCGACACAGCGTCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGCTGCACAATGTCACACCCGGGTGCCAAACACTTGGCCCCGGCGGCGACCCGGCCCTACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db 165786 CTGGCGGGCGAGCCCCGCGGGCGGGCTGGCGAGCGGGTGATGTCACGGGCAGCGGTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   481 CTCCTGCCGCCGCTCTCCGCGTCTCC-GGGGGAGGTGGCCCGGTTCGGCCGGGCAGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGGCGGGCGAGCCCCCGGGGCGGGCTGGCGAGCGGGTGATGTCACGGGCAGCGGTGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGGTCACTCGGAGGTGAGGCGCCCGCCAGGCGAGTTCAGCGAGAGTTCAGCCGCATTGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 188574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      504 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                     /clone_lib="RPCI_11 Human Male BAC"
1. 2072
/note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96.3%; Score 962.6; DB 2;
98.9%; Pred. No. 2.1e-186;
11ve 0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vector_side:right"
48660 c 47029 g 43760 t
                                                                                                                                                                                               /note-"assembly_fragment"
19449. 34798
/note-"assembly_fragment"
34899. 74660
/note-"assembly_fragment"
74761. 151113
/note-"assembly_fragment"
151214. 188574
/note-"assembly_fragment"
/clone="RP11-1029L16"
                                                                                                                                       vector_side:left"
2173. .19348
                                                                                                               clone_end: SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clone_end:T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 990; Conservative
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                                                                                                                                                                                                                       COMMENT
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B stren, B. Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barren, B., Nusbaum, C., Lander, E., Boukhqalter, B., Barna, N., Eastien, V., Bloom, T., Boquslavkiy, L., Boukhqalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Rado, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Lilev, I., Johnson, R., Lindblad-Toh, K., Karatas, A., Kells, C., Landers, T., Mangor, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C., Macdonald, P., Major, J., Matthews, C., Marchy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Peterson, R., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schubback, R., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Ramer, A. and Zody, M., Zamen, S., Severy, P., Lester, Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC126392 190309 bp DNA linear HTG 06-AUG-2002 Homo sapiens chromosome 17 clone RP11-1029F16 map 17, WORKING DRAFT SEQUENCE, 11 ordered pieces.
                           DD 165606 CCCCCTTCCCCCCCCCACCACCTCCACCACGGCTTCGCTCGGCCAGGGACTGACC 165547
                                                                                                                                                     Db 165546 AAACCTTGGGGGAGCCTGGGAGCCGGAACTGGTACAA-GGGAGGACGCCCGCCCCTCTTC 165488
                                                                                                                                                                                                                                     Db 165487 CGTCCTTGTCCCTCGCAGCCCCTCTCTCCCTGTACTCGGCGTCCCTCTGTACTCTGT 165428
                                                                                                                                                                                                                                                                                                                                                                       GTACTCCTCATCTGGAGCCTTTCCCCCTTCCTGCTTCTCTCCTCCTCCTCCCCTTCCCAG 165368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Euteleostomi;
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O'Connor, T., O'Donnell, P., O'Nell, D., Oliver, J., Peterson, K.,
                                                                                                                                                                                                                    899
                                                                                                                                                                                                                                                                                                                             959
720 CCCCCTCTTCCCCGCCCCACCTCCTCCACGACGGCTTCGCTCGGCCAGGGACTGACC 779
                                                                                                      840 CGTCCTTGTCCCCTCGCAGCCCCTCTCTCCTTGTACTCGGCGTCCCTCTGTACTCTGT
                                                                                                                                                                                                                                                                                                                     900 GTACTCCTCATCTGGAGCCTTTCCCCCTTCTTCTTCTCTTCTTCTTCCTCCCCCTTCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 199309)
Birren, B., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 17, clone RP11-1029F16
                                                                                                                                                                                                                                                                                                                                                 DD 165367 GCTGCCCCCACTTGCCTGTCCACATGCCGCCTCTCCCTCTC 165327
                                                                                                                                                                                                                                                                                                                                                                                                                           HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AC126392.2 GI:22123095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 190309)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
AC126392/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOURCE
ORGANISM
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TITLE
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Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

L. Submitted (06-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 6, 2002 this sequence version replaced 91:21699357.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: sequence_submissions@genome.wi.mit.edu
contact: sequence_submissions@genome.wi.mit.edu
center project information
Center project information
Center project name: L27553
Center clone name: 1029_r16
Consensus quality: 188131 bases at least Q30
Consensus quality: 188133 bases at least Q30
Consensus quality: 188537 bases at 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51471 66014: contrg of 100 bp
66015 66114: gap of 100 bp
66115 108183: contrg of 42069 bp in length
108184 108283: gap of 100 bp
108284 130510: contrg of 22227 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            108284 130510: contig of 22227 bp in length 130511 130610: gap of 100 bp 130511 16640: contig of 36130 bp in length 166741 166840: gap of 100 bp 166841 190309: contig of 23469 bp in length. Location/Qualiflers
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66014: contig of 14544 bp in length
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30614 31764: contig of 1151 bp in length
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33693: contig of 1829 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center code: WIBR
Web site: http://www-seq.wi.mit.edu
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Saltren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Baldwin, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellana, K., Demino, M., Donalan, L., Doule, M., Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lehockky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., Morkenan, K., McLaughlin, J., Meldrim, J., McTereira, P., Fileu, C., Locke, K., Macdonald, P., Marquis, N., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirreil, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Direct Submission N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirreil, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Direct Submission and Zody, M.

N. Stongerthos Street, Cambridge, MA 02141, USA On Jul 8, 2001 this sequence version replaced gi:13123358.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HTG 08-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC015851 158766 bp DNA linear HTG 08-JUL-2003
Homo sapiens chromosome 17 clone RP5-1112G21 map 17, WORKING DRAFT
SEQUENCE, 10 unordered pieces
167465 GGGTCACTCGGAGGTGAGGCGCCGCCAGGCGAGTTCAGCGAGAGTTCAGCCGCATTGCAT 167406
                                                                                                                                                                                                                                                                                                                                                                                     Db 167226 CGTCCTTGTCCCCTCGCAGCCCCTCCTCTGTACTCGGCGTCCCTGTACTCTGTACTCTTTT 167167
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Center: Whitehead Institute/ MIT Center for Genome Research
                                                                  DD 167405 TAGGCAAATGAGGCCCGGCCTGGGTGGGGTGTGTTTAAGGGGAGGACCACCGGGACCAC
                                                                                                                                                     D 167285 AAACCITGGGGGAGCCTGGGAGCCGGAACTGGTACAA-GGGAGGACGCCCCCCCTTTC
                                            TAGGCAAATGAGGCCCGGCCTGGGTGGGGTGTGTGTTAAGGGGAAGACACCGGGACCAC
                                                                                                                              720 CCCCCTCTTCCCCGCCCCACCACCTCCTCCACGGCTTCGCTCGGCCAGGGACTGACC
                                                                                                                                                                                                                   840 CGTCCTTGTCCCCTCGCAGCCCCTCTCTCCCTGTACTCGGCGTCCCTCTGTACTCTGT
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 189766)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 17, clone RP5-1112621
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Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC015851
AC015851.6 GI:14626914
HTG: HTGS_PHASE1; HTGS_BRAFT; HTGS_FULLTOP
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Center clone name: 1112_6_21
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Pred. No. 2.1e-186;
0; Mismatches 9;
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98.9%;
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Best Local Similarity 98.9°
Matches 990; Conservative
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Sequencing vector: M13; M77815; 41% of reads
Sequencing vector: Plasmid: L08752; 4% of reads
Sequencing vector: Plasmid: L08752; 4% of reads
Sequencing vector: Plasmid: L08752; 4% of reads
Chemistry: Dye-primer-amersham: 12% of reads
Chemistry: Dye-terminator Big Dye; 88% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 153948 bases at least Q40
Consensus quality: 155160 bases at least Q30
Consensus quality: 157160 bases at least Q20
Insert size: 63000; agarose-fp
Insert size: 157866; S.
* NOTE: This is "Working draft' sequence. It currently
* consists of 10 contigs. The true order of the pieces
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
                                                                                                                                                                                                                                                       1 2674: contig of 2674 bp in length
2675 2774: gap of 100 bp
2775 3397: contig of 623 bp in length
3398 497: gap of 100 bp
4543 4642: gap of 100 bp
4643 6062: gap of 100 bp
5963 6062: gap of 1320 h-
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1. .2671
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914 others

38051

BASE COUNT ORIGIN

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                                         Gaps
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                                                                                GTCCTTGGGTAGCATGTACATTTCCATCCTTCTTTATATATGGGGGTAATAGGATAC
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Score 956.8; DB 2;
Pred. No. 3.2e-185;
0; Mismatches 12;
Query Match
Best Local Similarity 98.5%;
Matches 987; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 241
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Contact: humquery@sanger.ac.uk
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AL591067.27 GI:22204212
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1833 bp DNA linear PRI 23-JUL-2000
Homo sapiens retinoic acid receptor alpha 2 isoform (RARA) gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MYESVEVGGPTPNPFLVVDFYNQNRACLLPEKGLPAPGPYSTPL
                                                                                                                                                                                                              2. (bases 1 to 1833)
Chen.A., Petrie,K., Waxman,S. and Zelent,A.
Direct Submission
Submitted (30-50N-2000) Leukaemia Research Fund Centre, Institute
of Cancer Research, 237 Fulham Road, London SW3 6JB, UK
Location/Qualifiers
                                                                                                                Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 CCCCTCCTCCAGGGTATCCCCTCTTTCTAGGGACCTACCCAAGCTAGGCCTTTCTTCCA 120
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Chen, A., Petrie, K., Waxman, S. and Zelent, A.
Homo sapiens retinoic acid receptor alpha (RAR-alpha) gene,
promoter and 5' region of RAR-alpha 2 isoform
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="retinoic acid receptor alpha 2 isoform"
/protein_id="AAF87249.1"
/db_xref="GI:9392670"
                                                                                                                                                                                                                                                                                                                                                                                                                           'product-"retinoic acid receptor alpha 2 isoform'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="RAR-alpha 2; nuclear receptor"
/codon_start=1
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Pred. No. 1.8e-168;
0; Mismatches 14;
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                                                                                                                                                                                                                                                                                      1. .1833
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="17"
/map="17q12-q21.1"
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AF283809.1 GI:9392669
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/gene="RARA"
676. .>1833
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97.58;
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/gene="RARA"
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      RESULT 7
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AL591067 231248 bp DNA linear HTG 09-AUG-2002
Mus musculus chromosome 11 clone RP23-333D2, *** SEQUENCING IN
PROCRESS ***, 2 unordered pieces.
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Murinae; Mus
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                       420 AGCTGCACAATGTCACACCCGGGTGCCAAACACTTGGCCCCGGGGGGCCCGGGCCCTACGC 479
                                                                                                                                                                                                                                              900
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                                                                              AGCTGCACAATGTCACACCCGGGTGCCAAACACTTGGCCCCGGGGGCCCGGCCCTACGC 480
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
1 (bases 1 to 231248)
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Web site: http://www.sanger.ac.uk
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962 TGCCCCCACTTGCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93 GACCTACCCAAGCTAGGCCTTTCTTCCAGTGAAACGTGCATCCCGAGGGCTTCTAGGATG 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  437
            Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator: 1% of reads
Chemistry: Dye-terminator Big Dye; 98% of reads
Consensus quality: 231046 bases at least Q40
Consensus quality: 231133 bases at least Q20
Insert size: 231148; sum-of-contigs arcs 23254; 2.5% error; agarose-fp
Quality coverage: 11.13x in Q20 bases; sum-of-contigs Quality; coverage: 11.16x in Q20 bases; agarose-fp
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                                                                                                                                                                                                                                                              NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            153 AAGTAGTCCACTGGAAGGCACCAGCTCTTCCTTTTATCTCTCCAGAGCTGGACAGTGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     137766 AAGTGCTTCAACTTAAGTC-----TCCTTTTATCTGTCCTGGGCT-----
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llarity 65.1%; Pred. No. 6.4e-44;
Conservative 0; Mismatches 248; Indels 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                   134201: contig of 134201 bp in length
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/note="assembly_fragment:06314"
/134302 .231248
/note="assembly_fragment:07956"
56205 c 57206 g 62207 t 1
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/organism="Mus musculus"
/db_xref="taxon:10090"
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/clone="RP23-333D2"
Statistics
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 1330)

S Leroy, P., Nakshatri, H. and Chambon, P. MOUGE RETINOIC ACID RECEPTOR ALPHA-2 ISOFORM IS TRANSCRIBED FROM A PROWOTOR THAT CONTAINS A RETINOIC ACID RESPONSE ELEMENT Proc. Natl. Acad. Sci. U.S.A. (1991) In press

E 2 (sites)

S Leroy, P., Nakshatri, H. and Chambon, P. Mouse retinoic acid receptor alpha 2 isoform is transcribed from a promoter that contains a retinoic acid response element

Proc. Natl. Acad. Sci. U.S.A. 88 (22), 10138-10142 (1991)
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Db 138039 CCCGGGACACCCAGCATGCTGCATTCGTGGTTCTAACGCTGGGCCACCTGCAATTGGGCC 138098
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retinoic acid receptor-alpha-2-isoform.
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    /organism="Mus musculus'

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         Gaps
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highly similar
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Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
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t lothers
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Homo sapiens trachea cDNA to mRNA, clone_lib:TRACH2
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                                                                                                                                                                                                                                                                 construct,
     DNA
                                                                                                                                                  Olek,A., Piepenbrock,C. and Berlin,K. Diagnosis of diseases associated with Patent: WO 0200927-A 216 03-JAN-2002; Epigenomics AG (DE)
 Sequence 216 from Patent W00200927. AX344791
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                                                                                                                                                                                               Isogai, T. and Yanamoto, J.

Direct Submission

Direct Submission

Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7

Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan

KE-mail:genomics@hri.co.jp, Tel:81-438-52-3956; Fax:81-438-52-3966;

KEOD human CDNA sequencing project supported by Ministry of

Economy, Trade and Industry of Japan; CDNA full insert sequencing:

Research Association for Biotechnology (RAB); CDNA library

CONSTRUCTION: Helix Research Institute (HRI) (supported by Japan

Key Technology Center etc.); 5'- 6 3'-end one pass sequencing: RAB,

HRI, and Biotechnology Center, National Institute of Technology and

Evaluation; clone selection for full insert sequencing: HRI and

RAB; annotation: HRI and RAB.

Location/Qualifiers
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Kataoka, R., Kuga, N., Kuroda, A., Satoh, I., Kamata, K., Takami, S., Terashima, Y., Matanabe, M., Sugiyama, T., Irie, R., Otsuki, T., Satoh, H., Ota, T., Wakamatsu, A., Ishi, S., Yamanoto, J., Isono, Y., Kawai Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Murakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K., and Isogai, T.
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100.0%; Pred. No. 1.5e-36;
tive 0; Mismatches 0;
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Sequence 215 from Patent WO0200927.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="TRACH2015486"
/tissue_type="trachea"
/clone=lib="FRACH2"
/note="cloning vector: ph
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Nature 1 (bases 1 to 162393)

Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allan, C., Ameroks, S.L., Amaraunge, M.C., Are, J.R., Aylele, M., Banks, T., Barbaria, J., Benton, J., Binge, K., Blankenburg, K., Bonnin, D., Bunbay, C., Burch, D., Burkett, C., Burchl, K.L., Byrd, N.C., Caron, T.E., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Caron, T.E., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Cord, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.D., Davis, C., Davila, M.D., Dathorne, S.R., David, R., Davila, M.D., Dayla, M.D., Dayla, M.D., Dayr-Carroll, L., Dederich, D.A., David, R.J., Delaney, K.R., J., Draper, H., Dugar-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Garner, T., Garsa, N., Garner, T., Garsa, N., Harnis, M., Haris, R., Harnis, K., Harris, K., Harris, K., Haves, A., Hamellton, K., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homs, J., Jia, Y., Johnson, R., Johloway, S., Hume, J., Jackson, L. E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,
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***, 72 unordered pieces.
AC111746.2 GI:21736893
HTC; HTGS_PHASEI.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     686 GGGGTGTGTTAAGGGGAGGACACCGGGACCACCCCCCTCTTCCCCGCCCCCACCACCTC 745
                                                                                                                                                                                                                                                                                                                            626 AGGCGAGTTCAGCGAGAGTTCAGCCGCATTAGCCAAATGAGGCCCGGCCTGGGTG 685
                                                               /note="chemically treated genomic DNA (Homo sapiens)"
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                                                                                                                                                                                       Score 143.8; DB 6;
Pred. No. 1.8e-19;
0; Mismatches 137;
/organism="synthetic construct"
/db_xref="taxon:32630"
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63.28;
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NOTE: This is a "working draft' sequence. It currently consists of 72 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Worley, K.C.
Direct Submission
Submitted (19-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 162393)
Worley, K.C.
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Direct Submission
Submitted (13-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jul 12, 2002 this Sequence version replaced gi:18701588.

Center: Baylor College of Medicine
Center: Baylor College of Medicine
Web Site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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Cheung,E., Medigue,C. and Danchin,A.
Exploring the Penicillium marneffei genome
Unpublished
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Matches 254;
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ACCESSION
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REFERENCE
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Danchin, A. and Pascal, G.
Direct Submission
Submitted (08-MAR-2002) Danchin A., HKU-Pasteur Research Centre,
Dexter HC Man Building 8, Sassoon Road, Pokfulam, Hong Kong
Location/Qualifiers
1. 972
                                                                                                                                                                                                                                                                        489 GCCGCTCTCCCCCGTCTCCCGGGGAGGTGGCCCGGTTCGGCCGGGCCAGGGGGCTGGCGGGC 548
                                                                                                                                                                                                                                                                                                         609 GGAGGTGAGGCGCCCCCAGGCGAGTTCAGCGAGAGTTCAGCCGCATTGCATTAGGCAAAT 668
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Dorner,F., Schoiflinger,F. and Falkner,F.Gunter.
Recombinant fowlpox virus
Patent: US 5670367-A 14 23-SEP-1997;
Location/Qualifiers
                                                                                                                                                    137
                                                                                                 /organism="Penicillium marneffei"
/db_xref="taxon:37727"
                                                                                                                                                                                                                                    0; Mismatches 291;
                                                                                                                                                                                                    Score 73.8; DB 11;
Pred. No. 4.3e-05;
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Sequence 14 from patent US 5670367.
166494.1 GI:2724471
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                                                                                                                                                           766 GCCAGGGACTGACCAAACCTTGGGGGGGGCCTGGGAGCCGGAACTGGTACAAGGGGAGGAC 825
                               Gaps
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Query Match 7.3%; Score 72.6; DB 6; Length 7218; Best Local Similarity 11.5%; Pred. No. 6.2e-05; Matches 27; Conservative 142; Mismatches 66; Indels 0.
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Job time : 2702.41 secs
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

March 30, 2003, 07:57:38 ; Search time 196.103 Seconds
(without alignments)
11483.757 Million cell updates/sec Run on:

1 gtecttgggtageatgtaca......acatgeegeeteteeetete 1000 US-09-691-220-3_COPY_1_1000 1000 Title: Perfect score: Sequence:

Scoring table:

2185239 seqs, 1125999159 residues IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Searched:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

1: SIDS2/gcgdata/geneseq/genesegn-embl/NA1980.DAT:*
2: SIDS2/gcgdata/geneseq-genesegn-embl/NA1981.DAT:*
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117: SIDS2/gcgdata/geneseq-genesegn-embl/NA1991.DAT:*
118: SIDS2/gcgdata/geneseq-genesegn-embl/NA1991.DAT:* N_Geneseq_101002

/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*/ /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1996. /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1997.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1998.DAr:*/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:* /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*

SUMMARIES

Description	Genomic DNA encodi Human chemically m Human proll gene. Human PKD1 gene. Human pCD1 jone. Human pCD1 locus b Human adenosine Al
a	AAL3339 ABN80199 ABN80198 AAD30228 AAT94101 AAT94108 AAX5491 AAX5491
DB	24 24 24 119 119 20
% Query Match Length DB ID	100.0 24.3 13508 14.4 13508 5.9 5.9 5.9 5.9 5.7 5.9 5.7 5.7 5.7 5.7 5.7 5.7 5.7 5.7 5.7 5.7
% Query Match	100.0 24.3 14.3 5.9 9.5 9.5 9.5 7.5 7.5
Score	1000 242.8 143.8 59.2 59.2 59.2 59.2 56.8 56.8
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ABA AAI ABC ABC ABC ABC	AAA AAA	AAA AABC AAAX ABN	ABC ABC ABC ABC	ABC ABC ABC ABC ABC ABC	AB040 AAT35 AAH26 ABA07
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ALIGNMENTS

/*tag= a /product= "Human nuclear hormone receptor protein" 1684..1846 Human nuclear hormone receptor; therapeutic agent; gene therapy; immune response; chromosome 17; single nucleotide polymorphism; gene; ds. Genomic DNA encoding the human nuclear hormone receptor protein. Location/Qualifiers 1684..15208 BP. AAL38339 standard; DNA; 20512 /number= 1 1847..6808 /*tag= c /number 1 6809..6957 /*tag d /number 2 6958..8277 /*tag e /number 2 (first entry) *tag= b Homo sapiens 15-AUG-2002 AAL38339; intron intron exon exon AAL38339

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The invention relates to an isolated peptide of a novel human nuclear hormone receptor with a fully defined sequence of 457 amino acids given in the specification. The novel human nuclear hormone receptor peptides and nucleic acids encoding them can be used as models for the development of human therapeutic of human therapeutic targets, aid in the identification of therapeutic of human therapeutic agents that modulate nuclear hormone receptor activity in cells and tissues that express the nuclear hormone receptor activity in cells and tissues that express the nuclear hormone receptor. The nucleic acids may be used as a query sequence to perform searches against sequence databases to identify family members or related sequences, as probes or primers, to construct recombinant vectors, to identify compounds that modulate nuclear hormone receptor nucleic acid expression, in gene therapy, and as antisense constructs to control nuclear hormone receptor gene expression in cells, tissues or organisms. The polypeptides can be used to raise antibodies or to elicit an immune response, as a reagent in assays designed to determine protein levels in biological fluids, as markers for tissues in which a corresponding protein is expressed, to identify a binding partner/ligand to develop a system for the clentification of inhibitors of the binding reaction, in drug screening assays, and to identify compounds the memoral protein activity. This polynucleotide sequence represents the genomic DNA encoding the human polynucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 CCCCTCCTCCAGGGGTATCCCCTCTTTCTAGGGACCTACCCAAGCTAGGCCTTTCTTCCA 120
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         Claim 1; Fig 3; 73pp; English.
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The invention relates to a nucleic acid (I) comprising a sequence at least 18 bases in length of a segment of chemically pretreated DNA (II) of genes associated with development selected from 87 genes listed in the specification such as ACCPN, ADFN, or AFDI and comprising one of 350 sequences (ABN79984-ABN80333) or their complements. The invention is useful for the diagnosis or therapy of diseases associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel nucleic acid useful for diagnosis and therapy of diseases associated with development genes such as diabetes, comprises a sequence of a segment of chemically pretreated DNA of genes associated
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                         CCCCTCTTCCCCGCCCCACCACCTCCTCCACGGCTTCGCTCGGCCAGGGACTGACCA
                                                                                                                                       601 GGTCACTCGGAGGTGAGGCGCCGCCAGGCGAGTTCAGCGAGAGTTCAGCCGCATTGCATT
                                                                                       AACCITGGGGAGCCTGGGAGCCGGAACTGGTACAAGGGGAGGACGCCCCGCCCTCTTCC
                                                                                                                                                                              GTCCTTGTCCCCTCGCAGCCCCCTCCTCTCCTGTACTCGGCGTCCCTCTGTACTCTGTG
                                                                                                                                                                                                                                TACTCCTCATCTGGAGCCTTTCCCCCTTCCTGCTTCTCTCCTCCTCCCCCTTCCCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human chemically modified disease associated gene SEQ ID NO 216
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development genes, in particular disease related to homeobox containing genes (HOX), like diabetes, cancer, apoptosis related diseases, syndromes associated with congenital heart disease, epilepsy, diseases related to histone deacetylation, Currarino syndrome, diseases related with the development of the brain and limb girdle muscular dystrophy and dwarfism. Oligomers specific to each of the genes are useful for detecting the methylation state of all CPG dinucleotides within the 350 sequences or (II) and their complementary sequences, as primer oligonucleotides for the amplification of the 350 sequences, (II) and/or their complements and as oligomer probes for detecting the cytosine methylation state and/or single nucleotide polymorphisms (SNPS).

Note: The sequence data for this parent did not form part of the printed specification but is based on sequence information supplied to Derwent by
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                                                                                                                                                                                                                                                                                                         DB 24; Length 13508;
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                                                                                                                                                                                                                                                                      Sequence 13508 BP; 3338 A; 286 C; 3789 G; 6094 T; 1 other;
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                                                                                                                                                                                                                                                                                                     Query Match 24.3%; Score 242.8; DB 2
Best Local Similarity 80.3%; Pred. No. 8.3e-45;
Matches 297; Conservative 0; Mismatches 72
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AAD30228 standard; DNA; 53522 BP

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The invention relates to a nucleic acid (I) comprising a sequence at least 18 bases in length of a segment of chemically pretreated DNA (II) of genes associated with development selected from 87 genes listed in the specification such as ACCPN, ADRN, or AFD1 and comprising one of 350 sequences (ABN79984-ABN80333) or their complements. The invention is useful for the diagnosis or their complements. The invention is development genes, in particular disease related to homeobox containing genes (HOX), like diabetes, cancer, apoptosis related diseases, syndromes associated with congenital heart disease, epilepsy, diseases related to histone deacetylation, Currarino syndrome, diseases related to histone deacetylation, Currarino syndrome, diseases related to dispensers specific to each of the genes are useful for detecting the methylation state of all CPG dinucleotides within the 350 sequences or (II) and their complementary sequences, as primer oligonucleotides for the amplification of the 350 sequences, as primer oligonucleotides for the amplification of the 350 sequences, as primer oligonucleotides for single nucleotide polymorphisms (SNPs). (II) and/or their complements and so oligomer probes for detecting the cytosine methylation state and/or single nucleotide polymorphisms (SNPs).

Whose: The sequence data for this patent did not form part of the printed specification but is based on sequence information supplied to Derwent by the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ä
                                                                                                                                                                                                                                                                                                                                                            Novel nucleic acid useful for diagnosis and therapy of diseases associated with development genes such as diabetes, comprises a sequence of a segment of chemically pretreated DNA of genes associated with development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6959 TTTTATTACGGTTTCGTTAGGGATTGATTAAATTTTGGGGGAGTTTGGGAGGTCGG 7018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6839 AGGGTAGTTTAGCGAGAGTTTAGTCGTATTGTATTAGGTAAATGAGGTTCGGTTTGGGTG 6898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7019 AATTGGTATAA-GGGAGGACGTTCGTTTTTTTCGTTTTTTCGTAGTTTTTT 7077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 686 GGGGTGTGTGTTAAGGGGAGGACACCGGGACCACCCCCTCTTCCCCGCCCCACCACCTC 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       806 AACTGGTACAAGGGAAGGACGCCCCCCTCTTCCGTCCTTGTCCCTCGCAGCCCCCTC 865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     626 AGGCGAGTTCAGCGAGAGTTCAGCCGCATTGCATTAGGCAAATGAGGCCCGGCCTGGGTG 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             746 CICCACCACGCTICGCTCGCCACGGACTCACCAAACCTTGGGGGAGCCTGGGAGCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     866 CTCTCCCTGTACTCGGCGTCCCTCTGTACTCTGTACTCCTCATCTGGAGCCTTTCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTTCCTGCTTCTCTCCTCCTCCCCCTTCCCAGGCTGCCCCCACTTGCCTGTCCACATG
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14.4%; Score 143.8; DB 24; Length 13508;
Best Local Similarity 63.2%; Pred. No. 1.1e-22;
Matches 237; Conservative 0; Mismatches 137; Indels 1: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 13508 BP; 2350 A; 286 C; 4030 G; 6841 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 1.1e-22;
0; Mismatches 137; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 215; 27pp; English.
                                                                                                                                                                                                           Berlin K;
30-JUN-2000; 2000DE-1032529.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7198 TCGTTTTTTTTTTC 7212
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                                                                                                                        (EPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                                                                                  WPI; 2002-130908/17.
                                                                                                                                                                                                   Olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       926
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The present invention relates to compositions and methods useful for the identification and detection of polycystic kidney disease (PKD1) gene mutations. The invention also relates to primers comprising a 5' region having a sequence that selectively hybridises to a PKD1 gene sequence and on optionally, to a PKD1 homologue sequence and an adjacent 3' region having a sequence that selectively hybridises to a PKD1 gene sequence and not to a PKD1 homologue sequence. Primer pairs of the invention are useful for detecting the presence or absence of a mutation in a PKD1 cuseful for detecting the presence or absence of a mutation in a PKD1 polyuncleotide in a sample, for identifying a subject at risk for a PKD1-associated disorder such as autosomal dominant polycystic kidney disease (ADPKD) or acquired cystic disease and for diagnosing a PKD1-associated disorder in a subject. They are useful for selectively aspititying a region of a PKD1 gene. PKD1 DNA fragments are useful cetecting the presence of a mutant PKD1 polynucleotide in a sample, as a probe for an amplification reaction, in hybridisation or amplification assays of biological samples to detect abnormalities of PKD1 expression and for engineering transgenic animals. The present sequence is human PKD1 gene chromosome 16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel primer for diagnosing polycystic kidney disease-associated disorder, comprises regions having sequence that selectively hybridizes to polycystic kidney disease gene sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; PKD1 gene; autosomal dominant polycystic kidney disease; ADPKD; acquired cystic disease; transgenic animal; chromosome 16; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      825 GGCCGGCCCTCTTCCGTCCTTGTCCCTCGCAGCCCCCTCTCTTCCTGTACTCGGCGT 884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     885 CCCTCTGTACTCTGTACTCCTCATCTGGAGCCTTTCCCCCTTCCTGCTTCTCCTCT 944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35529 CCTCCCCTCCTTCCCCCTCCTCCTTCTCCCCATCCCCCTTCTC 35584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             945 CCTCCCCCTTCCCAGGCTGCCCCACTTGCCTGTCCACATGCCGCCTCTCCCTCTC 1000
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58.5%; Pred. No. 0.0011;
tive 0; Mismatches 73; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 53522 BP; 8486 A; 17664 C; 15766 G; 11606 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 20; Page 127-156; 192pp; English.
                                                                                                                                                                                                                                                                                                                                                                            2000US-218261P.
2001US-283691P.
                                                                                                                                                                                                                                                                                                                                  13-JUL-2001; 2001WO-US22035.
                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Watnick TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 5.9
Best Local Similarity 58.5
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-179805/23.
                                                                                              Human PKD1 gene.
                                                                                                                                                                                                                                               WO200206529-A2.
                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                            13-JUL-2000;
13-APR-2001;
                                                         17-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Germino GG,
                                                                                                                                                                                                                                                                                           24 - JAN - 2002
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/*tag= a
/note= "specifically claimed region of intronless
cDNA identified by exon trapping"
replace(50652..50653, cg)

Location/Qualifiers 4379..5272

to Leu codon"

/*tag= b /note= "changes Val codon replace(50796..50797, cg)

/*tag= d /note= "insertion, results in frameshift"

95WO-US13357. 95US-0381520 94US-0323443

dominant;

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Isolated human polycystic kidney disease gene and its mutants useful for treatment of polycystic kidney disease and screening for
                                                    Adult onset polycystic kidney disease; APKD; autosomal mutant; transversion; transition; deletion; insertion;
                               Human polycystic kidney disease normal PKD1 gene.
                                                                                                                                                                                                                                                                                                                                                                                    UYJO ) UNIV JOHNS HOPKINS
                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1996-222017/22
                                                                                                                                                                                                                                                                                                                                                                        IGIG-) IG LAB
                                                                                       Homo sapiens
                                                                                                           Key
misc_feature
                                                                                                                                                               old_sequence
                                                                                                                                                                                                                                                                           WO9612033-A1
                                                                                                                                                                                                 old_sequence
                                                                                                                                                                                                                                                                                                                                                     12-OCT-1994;
                                                                                                                                                                                                                              old_sequence
          06-MAY-1997
                                                                                                                                                                                                                                                                                                                      11-OCT-1995;
                                                                                                                                                                                                                                                                                                                                           31-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                    η TC,
' GM,
                                                                                                                                                                                                                                                                                                25-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                      Landes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          885 CCCTCTGTACTCTGTACTCCTCATCTGGAGCCTTTCCCCCTTTCCTGCTTCTCTCCTCT 944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Phe present sequence is the human polycystic kidney disease l (PKD1) gene. The PKD1 gene or polypeptide may be used to treat autosomal dominant polycystic kidney disease (APKD), and identify carriers of mutant PKD1 genes, i.e. subjects susceptible to APKD. Antibodies (AD) that distinguish between normal and mutant PKD1 sequences can also be used in diagnostic tests. Anti-PKD1 AD may also be used to perform subcellular and histochemical localisation studies, and to block the function of PKD1. Ab are also useful in rational drug design studies to identify and test inhibitors of PKD1. Sense and antisense sequences derived from the PKD1 gene may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    945 CCTCCCCCTTCCCAGGCTGCCCCCACTTGCCTGTCCACATGCCGCCTCTCCCTCTC 1000
                                                                                                                                                                                                                                                                                                                                            Human polycystic kidney disease gene, PKD1 - useful to treat and diagnose human autosomal or adult onset polycystic kidney disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5.9%; Score 59.2; DB 19; Length 53526; llarity 58.5%; Pred. No. 0.0011; Conservative 0; Mismatches 73; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 53526 BP; 8486 A; 17665 C; 15768 G; 11607 T; 0 other;
                                                                                                                                                                                                                                                                                            Dackowski W, Germino G, Klinger K;
                                                                                                            Human; polycystic kidney disease 1; PKD1; treatment; autosomal dominant polycystic kidney disease; APKD; ss.
                                                                                                                                                                                                                                                                                                                                                                            Claim 2; Pages 90-118; 257pp; English.
                       AAT94101 standard; DNA; 53526 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for detection and therapy.
                                                                                                                                                                                                                                    96US-0658136.
                                                                                                                                                                                                               97WO-US08799
                                                                  01-JUN-1998 (first entry)
                                                                                                                                                                                                                                                                    (GENZ ) GENZYME CORP.
                                                                                                                                                                                                                                                                                          Connors T,
                                                                                                                                                                                                                                                                                                                        WPI; 1998-018511/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                       Human PKD1 gene
                                                                                                                                               Homo sapiens
                                                                                                                                                                                                               22-MAY-1997;
                                                                                                                                                                                                                                   03-JUN-1996;
24-MAY-1996;
                                                                                                                                                                  WO9744457-A1
                                                                                                                                                                                         27-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 103;
                                              AAT94101;
                                                                                                                                                                                                                                                                                        Burn T,
Qian F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
   RESULT 5
              AAT94101
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Klinger KW;

Germino G,

Dackowski W,

Connors TD,

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The present sequence is that of the normal human PKDI gene from chromosome 16, wutations in this gene (e.g. transitions, transversions, deletions and/or insertions) are associated with adult-onset polycystic kidney disease (APKD). The PKDI locus is GC-rich (62.4%). Comparison of this sequence with a previously reported partial cDNA sequence revealed differences at three locations (see features table). The most significant difference is the presence of two additional cytosine residues on the plus-strand at position 4566 of the previously reported sequence. The insertion essuits in a frame-shift in the predicted protein coding sequence. Cleading to replacement of 92 C-terminal amino acid with a novel consisting of 17 tandem copies of a perfect 27 bp repeat and two large CT-rich regions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCCCCCCCCTCTTCCGTCCTTGTCCCCTCGCAGCCCCTCCTCTCCCTGTACTCGGCGT 884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 17; Length 53577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 53577 BP; 8495 A; 17681 C; 15785 G; 11616 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.0011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.9%; Score 59.2; Dilarity 58.5%; Pred. No. 0.00 Conservative 0; Mismatches
Claim 1; Fig 1; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
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AAT18551 standard; DNA; 53577 BP.

RESULT 6
AAT18551
ID AAT1
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AC AAT1

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AAT18551;

Db 35528 CCTCCCCTCCCTTCCCCTCCCTTCTCCCCATCCCCCTTCTC 35583

BP

AAX53491/c ID AAX53491 standard; DNA; 114955

RESULT

Antisense oligonucleotide; multiple target; antisense treatment; impaired respiration; inflammation; lung disease; pulmonary vasoconstriction; inflammation; allergic rhinitis;

Human adenosine Al receptor antisense oligonucleotide fragment.

(first entry)

05-JUL-1999

AAX53491;

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Human PKD1 locus between chromosomal markers ATPL (ATP6C) and D16S84.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is the human polycystic kidney disease I (PKD1) locus between chromosomal markers ATPL (ATP6C) and D16S84. The PKD1 gene or polypeptide may be used to treat autosomal dominant polycystic kidney disease (APKD), and identify carriers of mutant PKD1 genes, i.e. subjects susceptible to APKD. Antibodies (Ab) that distinguish between normal and mutant PKD1 sequences can also be used in diagnostic tests. Anti-PKD1 Ab may also be used to perform subcellular and histochemical localisation studies, and to block the function of PKD1. Ab are also useful in rational drug design studies to identify and test inhibitors of PKD1. Sense and antisense sequences derived from the PKD1 gene may used for
                                                                        945 CCTCCCCTTCCCAGGCTGCCCCCACTTGCCTGTCCACATGCCGCCTCTCCTCTC 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human polycystic kidney disease gene, PKD1 - useful to treat and diagnose human autosomal or adult onset polycystic kidney disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 53577 BP; 8495 A; 17684 C; 15782 G; 11616 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Connors T, Dackowski W, Germino G, Klinger K;
                                                                                                                                                                                                                                                                                Human; polycystic kidney disease 1; PKD1; treatment; autosomal dominant polycystic kidney disease; APKD; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 5; Pages 60-89; 257pp; English.
                                                                                                                                                             AAT94108 standard; DNA; 53577 BP
                                                                                                                                                                                                                                                                                                                                                                                                                        97WO-US08799
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96US-0655360
                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-018511/02.
                                                                                                                                                                                                                                                                                                                                                         W09744457-A1
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                                                                                                                                                                                                                                                                                                                              Homo sapiens
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24-MAY-1996;
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                                                                                                                                                                                            AAT94108;
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885
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                                                                                                                                   RESULT
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The specification describes antisense oligonucleotides (AAX52869-X55271)

directed against at least 2 mRNAs selected from target genes, coding and
conditions and all sequence flanking regions, intron-exon borders, the
initiation codons, genomic flanking regions, intron-exon borders, the
conditions and all segments of RNAs encoding proteins associated with one
conditions and all segments of RNAs encoding proteins associated with one
cor more diseases, conditions or mixtures. The antisense oligonuclectides
cor more diseases, conditions or mixtures. The antisense oligonuclectides
cor more diseases, conditions or mixtures. The antisense oligonuclectides
antisense transment of diseases and conditions. Typical diseases and
conditions are those associated with impaired respiration and
conditions are those associated with impaired respiration and
inflammation, including lung diseases, pulmonary vasoconstriction,
condition, allergic rhinitis, acute asthma, allergies, asthma, impeded
respiration, respiratory distress syndrome, pain, cystic fibrosis,
cuspiration, pulmonary disease (COPD), and cancers such as leukemias,
lymphomas, carcinomas e.g. colon cancer, breast cancer, lung cancer,
constructive pulmonary disease (COPD), and cancers such as leukemias,
lymphomas, carcinomas e.g. colon cancer, breast cancer, lung cancer,
constructive pulmonary was well as all types of cancers which may metastasize
cor have metastasized to the lungs, including breast and prostate cancer.
acute asthma; allergy; asthma; impeded respiration; respiration; respiratory distress syndrome; pain; cystic fibrosis; pulmonary hypertension; pulmonary vasoconstriction; emphysema; chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma; colon cancer; breast cancer; lung cancer; pancreatic cancer; hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New antisense oligonucleotides used in treatment of, e.g. pulmonary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 114955 BP; 6071 A; 29417 C; 36712 G; 21328 T; 21427 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 37; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                      98WO-US19419.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0093972
97US-0059160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYEC-) UNIV EAST CAROLINA.
                                                                                                                                                                            prostate cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-229400/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vasoconstriction
                                                                                                                                                                                                                                                                                      WO9913886-A1
                                                                                                                                                                                                                                                                                                                                                                                                   17-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-SEP-1997;
                                                                                                                                                                                                                                                                                                                                             25-MAR-1999
                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nyce JW;
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7

Gaps

4;

Indels

Similarity 31.5%; Score 56.8; DB 20; Similarity 31.5%; Pred. No. 0.0043; 20; Conservative 77; Mismatches 397;

Matches 220; Conservative

Query Match Best Local S

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0;

Indels

DB 19; Length 53577;

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825 CGCCCGCCCTCTTCCGTCCTTGTCCCCTCGCAGCCCCCTCTCTCCTGTACTCGGCGT 884

5.9%; Score 59.2; DB 19; 58.5%; Pred. No. 0.0011; tive 0; Mismatches 73;

Best Local Similarity 58.5 Matches 103; Conservative

Ouery Match

945 CCTCCCCTTCCCAGGCTGCCCCACTTGCCTGTCCACATGCCGCCTCTCCCTCTC 1000

WO9913886-A1

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DD 104858 HNNNSCVGGCCVGCGGNNHNNNSCCVGGCCVGCGGNNHNNNSCCVGCGCGVGCGGNNHNN 104799
                                                                                                   104798 NSGCCCVGCGCONHNNNSCGCCCVGGCCVGCGCNNHNNNSGCGCCVGGCCVGCG 104739
                                                                                                                                                                           GNNHNNNSCGCGCCCVGGCCVGCGGNNHNNNSGCGCGCCCVGGCCVGCGGNNHNNNSGGC 104679
                                                                                                                                                                                                                                         GCGCCCVGGCCNGGCNNHNNNSCGGCGCGCCCVGGCCNGGNNHNNNSGCGGCGCGCC 104619
                                                                                                                                                                                                                                                                                                                        104618 CVGGC-CVGCGGNNHNNNSGGCGGCGCGCCVGGCCVGCGGNNHNNSCGGCGGCGCGCC 104560
                                                                                                                                                                                                                                                                                                                                                                                         CYGGCCYGCGGNNHNNNSCCGGCGCGCGCCCYGGCCAGGCGNNHNNNSGCCGGCGCGC 104500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCGGCGCGCCVGCGCNNHNNNSCCGGCGGGGGGCGCCCVGGCGCNNHN 104380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DD 104322 CCVGGCCVGCGGNNHNNNSGGCCCGGCGGCGCGCGCCCVGCGCNNHNNNSCGG 104263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DD 104262 CCCGGCCGCGCGCGCCCVGGCCVGCGGNNHNNNSGCCCGGCCCGNNHNNNSGCCCGCC 104203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTCTCCAGAGCTGGACAGTGCACCAGGGCCGGTACTGGTTCCCCCAGCTAGGAGACACCT 249
                                                                                                                                          GTGTTTGTGCCAACAGCACCCGCGTGCCGCGTCGGGTTCCGGCGGCCGGAGTCACACAT 369
                                                                                                                                                                                                                                                                                                                                                                                                                                          609
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pulmonary hypertension; pulmonary vasoconstriction; emphysema; chronic obstructive pulmonary disease; leukemia; lymphona; carcinoma; colon cancer; breast cancer; lung cancer; pancreatic cancer; hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
                                                                                                                                                                                                                 GATGTCACAGACAATGACACAAGCCGGTGTCTCATTCCGACACAGCGTCCGAGCTGCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                     104499 GCCCVGGCCVGCGGNNHNNNSGGCCGGCGCGCCCVGGCCVGCGGNNHNNNSCGGCCG
                                                                     TGGGCGGGGCTTTGCTCGCCGGAAGCACGCAGAGCGTGGGGAGGAGGGCCCCCTCTGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAGGTGAGGCGCCGCCAGGCGAGTTCAGCGAGAGTTCAGCCGCATTGCATTAGGCAAATG
                                                                                                                                                                                                                                                                                          ATGTCACACCCGGGTGCCAAACACTTGGCCCCGCGCGGCCCCTACGCCTCCTGCCG
                                                                                                                                                                                                                                                                                                                                                             AGGCCCGGCCTGGGTGGGGTGTGTTAAGGGGAGGACACCGGGACCACCCCCCTCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCCGCCCCACCACCTCCTCCACCACGGCTTCGCTCGGCCAGGGACTGACCAAACCTTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antisense oligonucleotide; multiple target; antisense treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human adenosine Al receptor antisense oligonucleotide fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      impaired respiration; inflammation; lung disease; pulmonary vasoconstriction; inflammation; allergic rhinitis; acute asthma; allergy; asthma; impeded respiration; respiratory distress syndrome; pain; cystic fibrosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db 104202 CCGANNHNNNSGCCCGGCCCGACNNHNNNSGCCCGGCC 104165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCCTCGCAGCCCCTCTCCCTGTACTCGGCGTCCC 887
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAX53491 standard; DNA; 114955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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The specification describes antisense oligonucleotides (AAX52869-X55271)

directed against at least 2 mRNAs selected from target genes, coding and
non-coding regions of RNAs corresponding to target genes, gene
initiation codons, genomic flanking regions, intron-exon borders, the
confidence diseases, conditions or mixtures. The antisense oligonucleotides
cor more diseases, conditions or mixtures. The antisense oligonucleotides
cor more diseases, conditions or mixtures. The antisense oligonucleotides
conditions are those associated with impaired respiration and
conditions are those associated with impaired respiration and
inflammation, including lung diseases, pulmonary vasoconstriction,
inflammation, allergic rhinitis, acute asthma, allergies, asthma, impeded
respiration, respiratory distress syndrome, pain, cystic fibrosis,
constructive pulmonary disease (COPD), and cancers such as leukemias,
lymphomas, carctionmas e.g. colon cancer, bepacter, lung cancer,
constructive pulmonary disease (COPD), and cancers such as leukemias,
lymphomas, carctionmas e.g. colon cancer, bepacter, melanoma,
conflammatic cancer, hepatocellular carcinoma, kidney cancer, melanoma,
chepatic metastasise, as well as all types of cancers which may metastasize
cor have metastasized to the lungs, including breast and prostate cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       104139 GCGTCGGGCCGGCSNNNDNNCGTCGGCCCGGCCNNNDNNGTCGCGCCGGCCSNNNDNN 104198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            104199 TCGGGCCGGGCSNNNDNNCGGGCCGGGCSNNNDNNCCGCBGGCCCGCGCCGCCGCC 104258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             104378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              371 ATGTCACAGACAATGACACAAGCCGGTGTCTCATTCCGACACAGCGTCCGAGCTGCACAA 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   251 GGGCGGGGCTTTGCTCGCCGGAAGCACGCAGAGCGTGGGGAGGAGGGCCCCCTCTGCCTG 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 611 AGGTGAGGCGCCCAGGCGAGTTCAGCGAGGTTCAGCCGCATTGCATTAGGCAAATGA 670
                                                                                                                                                                                                                                                                                                                                    antisense oligonucleotides used in treatment of, e.g. pulmonary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 114955 BP; 6071 A; 29417 C; 36712 G; 21328 T; 21427 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       104259 CGGCCCGSNNNDNNCCGCBGGCCCGGCCGCCGCCGGCCGGCCSNNNDNNCCGCBGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           311 TGTTTGTGCCAACAGCACCGGGGTGCCGCGTTCCGGGTGCGGCGGCGGAGTCACATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.4%; Score 54.4; DB 20;
30.0%; Pred. No. 0.015;
Live 68; Mismatches 429;
                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 37; 120pp; English
                                                                                     98WO-US19419
                                                                                                                             98US-0093972
97US-0059160
                                                                                                                                                                                                  (UYEC-) UNIV EAST CAROLINA.
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                                                                                                                                                                                                                                                                                     WPI; 1999-229400/19
                                                                                                                                                                                                                                                                                                                                                        vasoconstriction
                                                                                   17-SEP-1998;
                                                                                                                                                      7-SEP-1997;
                                                                                                                             09-JUN-1998;
                                         25-MAR-1999
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                                                                                                                                                                                                                                              Nyce JW;
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01-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antialiergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antiacterial; antimugal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein; ds.
Db 104439 CCGGCCGSNNNDNNCCGCBGGCCBGGCCGCCGCCGCCGCCSNNNDNNCCGCBGGCCBGGG 104498
                                                                  DD 104499 CGCGCCGCCGCCGNNNDNNCCGCBGGCCGCGCGCGCCGCCGCCGCCGCGCGCCG 104558
                                                                                                                                               Db 104559 GGGCGCCCCCCGSNNNDNNCCGCBGGCCBGGCCGCCCCCCNNNDNNCCGCBGGCCBG 104618
                                                                                                                                                                                                        DD 104619 GGCGCGCCGCSNNNDNNCCGCBGGCCBGGCCCGCGNNNDNNCCGCBGGCCBCGCGC 104678
                                                                                                                                                                                                                                                                                   Db 104679 GCCSNNNDNNCCGCBGGCCBGGCGCGCSNNNDNNCCGCBGGCCBGGCGGSNNNDNNC 104738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human ovarian and breast cancer associated polynucleotide SEQ ID NO 1003
                                               671 GCCCGGCCTGGGTGGGGTGTGTTAAGGGGAGGACACCGGGACCACCCCCCTTCC 730
                                                                                                                                                                                   851 CCTCGCAGCCCCCTCTCTCCCTGTACTCGGCGTCCCTCTGTACTCTGTACTCCTCAT 910
                                                                                                                731 CCGCCCCACCACCTCCTCCACCACGCTTCGCTCGGCCAGGGACTGACCAAACCTTGGGG
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2000US-0205515.
2000US-0209467.
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20000S-022527
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14-AUG-2000;
14-AUG-2000;
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ABA08208
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